



SEQUENCE LISTING

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<120> MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
ANTIBIOTICS

<130> OGZ-001

<140> 09/813,453

<141> 2001-03-20

<150> US 60/227,860

<151> 2000-08-24

<150> 09/667,569

<151> 2000-09-21

<160> 77

<170> PatentIn Ver. 2.0

<210> 1

<211> 777

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(774)

<400> 1

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1 5 10 15	
tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg	96
Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg	
20 25 30	
cat aaa aca gaa gat gag ttt ggg atg att ttg cgc tcc tta ttt gat	144
His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp	
35 40 45	
cac tcc ggg ctt atg ttt gaa cag ata gat ggc att att att tcg tca	192
His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser	
50 55 60	
gta gtg ccg cca atc atg ttt gcg tta gaa aga atg tgc aca aaa tac	240
Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr	
65 70 75 80	
ttt cat atc gag cct caa att gtt ggt cca ggt atg aaa acc ggt tta	288
Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu	
85 90 95	

aat ata aaa tat gac aat ccg aaa gaa gta ggg gca gac aga atc gta	336
Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val	
100 105 110	
aat gct gtc gct gcg ata cac ttg tac ggc aat cca tta att gtt gtc	384
Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val	
115 120 125	
gat ttc gga acc gcc aca acg tac tgc tat att gat gaa aac aaa caa	432
Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln	
130 135 140	
tac atg ggc ggg gcg att gcc cct ggg att aca att tcg aca gag gcg	480
Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala	
145 150 155 160	
ctt tac tcg cgt gca gca aag ctt cct cgt atc gaa atc acc cgg ccc	528
Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro	
165 170 175	
gac aat att atc gga aaa aac act gtt agc gcg atg caa tct gga att	576
Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile	
180 185 190	
tta ttt ggc tat gtc ggc caa gtg gaa gga atc gtt aag cga atg aaa	624
Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys	
195 200 205	
tgg cag gca aaa cag gac ctc aag gtc att gcg aca gga ggc ctg gcg	672
Trp Gln Ala Lys Gln Asp Leu Lys Val Ile Ala Thr Gly Gly Leu Ala	
210 215 220	
ccg ctc att gcg aac gaa tca gat tgt ata gac atc gtt gat cca ttc	720
Pro Leu Ile Ala Asn Glu Ser Asp Cys Ile Asp Ile Val Asp Pro Phe	
225 230 235 240	
tta acc cta aaa ggg ctg gaa ttg att tat gaa aga aac cgc gta gga	768
Leu Thr Leu Lys Gly Leu Glu Leu Ile Tyr Glu Arg Asn Arg Val Gly	
245 250 255	
agt gta tag	777
Ser Val	

<210> 2
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 <212> PRT
 <213> Bacillus subtilis

<400> 2
 Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1 5 10 15
 Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30

His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
 35 40 45
 His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
 50 55 60
 Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65 70 75 80
 Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
 85 90 95
 Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
 100 105 110
 Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
 115 120 125
 Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
 130 135 140
 Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
 145 150 155 160
 Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
 165 170 175
 Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
 180 185 190
 Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
 195 200 205
 Trp Gln Ala Lys Gln Asp Leu Lys Val Ile Ala Thr Gly Gly Leu Ala
 210 215 220
 Pro Leu Ile Ala Asn Glu Ser Asp Cys Ile Asp Ile Val Asp Pro Phe
 225 230 235 240
 Leu Thr Leu Lys Gly Leu Glu Leu Ile Tyr Glu Arg Asn Arg Val Gly
 245 250 255
 Ser Val

<210> 3
 <211> 250
 <212> PRT
 <213> Clostridium acetobutylicum

<400> 3
 Asn Lys Arg Ala Ala Phe Met Leu Leu Leu Phe Leu Arg Ser Val Leu
 1 5 10 15
 Lys Val Ile Leu Val Leu Asp Val Gly Asn Thr Asn Ile Val Leu Gly
 20 25 30

Ile Tyr Asn Asp Thr Lys Leu Thr Ala Glu Trp Arg Leu Ser Thr Asp
 35 40 45
 Val Leu Arg Ser Ala Asp Glu Tyr Gly Ile Gln Val Met Asn Leu Phe
 50 55 60
 Gln Gln Asp Lys Leu Asp Pro Thr Leu Val Glu Gly Val Ile Ile Ser
 65 70 75 80
 Ser Val Val Pro Asn Ile Met Tyr Ser Leu Glu His Met Ile Arg Lys
 85 90 95
 Tyr Phe Lys Ile Asn Pro Leu Val Val Gly Pro Gly Ile Lys Thr Gly
 100 105 110
 Ile Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile
 115 120 125
 Val Asn Ala Val Ala Ala His Glu Ile Tyr Lys Arg Ser Leu Ile Ile
 130 135 140
 Ile Asp Phe Gly Thr Ala Thr Thr Phe Cys Ala Val Arg Glu Asn Gly
 145 150 155 160
 Asp Tyr Leu Gly Gly Ala Ile Cys Pro Gly Ile Lys Val Ser Ser Glu
 165 170 175
 Ala Leu Phe Glu Lys Ala Ala Lys Leu Pro Arg Val Glu Leu Ile Lys
 180 185 190
 Pro Ala Tyr Ala Ile Cys Lys Asn Thr Ile Ser Ser Ile Gln Ser Gly
 195 200 205
 Ile Val Tyr Arg Tyr Leu Arg Gln Val Lys Tyr Leu Phe Glu Lys Leu
 210 215 220
 Lys Glu Asn Leu Pro Asp Gly Arg Arg Thr Arg Thr Ser Leu Val Leu
 225 230 235 240
 Ala Thr Gly Gly Leu Ala Lys Leu Ile Asn
 245 250

<210> 4
 <211> 265
 <212> PRT
 <213> Streptomyces coelicolor

<400> 4
 Met Leu Leu Thr Ile Asp Val Gly Asn Thr His Thr Val Leu Gly Leu
 1 5 10 15
 Phe Asp Gly Glu Asp Ile Val Glu His Trp Arg Ile Ser Thr Asp Ser
 20 25 30
 Arg Arg Thr Ala Asp Glu Leu Ala Val Leu Leu Gln Gly Leu Met Gly

35					40					45					
Met	His	Pro	Leu	Leu	Gly	Asp	Glu	Leu	Gly	Asp	Gly	Ile	Asp	Gly	Ile
	50					55					60				
Ala	Ile	Cys	Ala	Thr	Val	Pro	Ser	Val	Leu	His	Glu	Leu	Arg	Glu	Val
65					70					75					80
Thr	Arg	Arg	Tyr	Tyr	Gly	Asp	Val	Pro	Ala	Val	Leu	Val	Glu	Pro	Gly
				85					90					95	
Val	Lys	Thr	Gly	Val	Pro	Ile	Leu	Thr	Asp	His	Pro	Lys	Glu	Val	Gly
			100					105					110		
Ala	Asp	Arg	Ile	Ile	Asn	Ala	Val	Ala	Ala	Val	Glu	Leu	Tyr	Gly	Gly
		115					120					125			
Pro	Ala	Ile	Val	Val	Asp	Phe	Gly	Thr	Ala	Thr	Thr	Phe	Asp	Ala	Val
	130					135					140				
Ser	Ala	Arg	Gly	Glu	Tyr	Ile	Gly	Gly	Val	Ile	Ala	Pro	Gly	Ile	Glu
145					150					155					160
Ile	Ser	Val	Glu	Ala	Leu	Gly	Val	Lys	Gly	Ala	Gln	Leu	Arg	Lys	Ile
				165				170						175	
Glu	Val	Ala	Arg	Pro	Arg	Ser	Val	Ile	Gly	Lys	Asn	Thr	Val	Glu	Ala
			180					185					190		
Met	Gln	Ser	Gly	Ile	Val	Tyr	Gly	Phe	Ala	Gly	Gln	Val	Asp	Gly	Val
		195					200					205			
Val	Asn	Arg	Met	Ala	Arg	Glu	Leu	Ala	Asp	Asp	Pro	Asp	Asp	Val	Thr
	210					215					220				
Val	Ile	Ala	Thr	Gly	Gly	Leu	Ala	Pro	Met	Val	Leu	Gly	Glu	Ser	Ser
225					230					235					240
Val	Ile	Asp	Glu	His	Glu	Pro	Trp	Leu	Thr	Leu	Met	Gly	Leu	Arg	Leu
				245				250						255	
Val	Tyr	Glu	Arg	Asn	Val	Ser	Arg	Met							
		260						265							

<210> 5

<211> 272

<212> PRT

<213> Mycobacterium tuberculosis

<400> 5

Met	Leu	Leu	Ala	Ile	Asp	Val	Arg	Asn	Thr	His	Thr	Val	Val	Gly	Leu
1				5					10					15	
Leu	Ser	Gly	Met	Lys	Glu	His	Ala	Lys	Val	Val	Gln	Gln	Trp	Arg	Ile
			20					25					30		

Arg Thr Glu Ser Glu Val Thr Ala Asp Glu Leu Ala Leu Thr Ile Asp
 35 40 45
 Gly Leu Ile Gly Glu Asp Ser Glu Arg Leu Thr Gly Thr Ala Ala Leu
 50 55 60
 Ser Thr Val Pro Ser Val Leu His Glu Val Arg Ile Met Leu Asp Gln
 65 70 75 80
 Tyr Trp Pro Ser Val Pro His Val Leu Ile Glu Pro Gly Val Arg Thr
 85 90 95
 Gly Ile Pro Leu Leu Val Asp Asn Pro Lys Glu Val Gly Ala Asp Arg
 100 105 110
 Ile Val Asn Cys Leu Ala Ala Tyr Asp Arg Phe Arg Lys Ala Ala Ile
 115 120 125
 Val Val Asp Phe Gly Ser Ser Ile Cys Val Asp Val Val Ser Ala Lys
 130 135 140
 Gly Glu Phe Leu Gly Gly Ala Ile Ala Pro Gly Val Gln Val Ser Ser
 145 150 155 160
 Asp Ala Ala Ala Ala Arg Ser Ala Ala Leu Arg Arg Val Glu Leu Ala
 165 170 175
 Arg Pro Arg Ser Val Val Gly Lys Asn Thr Val Glu Cys Met Gln Ala
 180 185 190
 Gly Ala Val Phe Gly Phe Ala Gly Leu Val Asp Gly Leu Val Gly Arg
 195 200 205
 Ile Arg Glu Asp Val Ser Gly Phe Ser Val Asp His Asp Val Ala Ile
 210 215 220
 Val Ala Thr Gly His Thr Ala Pro Leu Leu Leu Pro Glu Leu His Thr
 225 230 235 240
 Val Asp His Tyr Asp Gln His Leu Thr Leu Gln Gly Leu Arg Leu Val
 245 250 255
 Phe Glu Arg Asn Leu Glu Val Gln Arg Gly Arg Leu Lys Thr Ala Arg
 260 265 270

<210> 6

<211> 258

<212> PRT

<213> Rhodobacter capsulatus

<400> 6

Met Leu Leu Cys Ile Asp Cys Gly Asn Thr Asn Thr Val Phe Ser Val
 1 5 10 15

Trp Asp Gly Thr Asp Phe Ala Ala Thr Trp Arg Ile Ala Thr Asp His
 20 25 30

Arg Arg Thr Ala Asp Glu Tyr Phe Val Trp Leu Asn Thr Leu Met Gln
 35 40 45
 Leu Lys Gly Leu Gln Gly Arg Ile Ser Glu Ala Ile Ile Ser Ser Thr
 50 55 60
 Ala Pro Arg Val Val Phe Asn Leu Arg Val Leu Cys Asn Arg Tyr Phe
 65 70 75 80
 Asp Cys Arg Pro Tyr Val Val Gly Lys Pro Gly Cys Glu Leu Pro Val
 85 90 95
 Ala Pro Arg Val Asp Pro Gly Thr Thr Val Gly Pro Asp Arg Leu Val
 100 105 110
 Asn Thr Val Ala Gly Tyr Asp Arg His Gly Gly Asp Leu Ile Val Val
 115 120 125
 Asp Phe Gly Thr Ala Thr Thr Phe Asp Val Val Ala Pro Asp Gly Ala
 130 135 140
 Tyr Ile Gly Gly Val Ile Ala Pro Gly Val Asn Leu Ser Leu Glu Ala
 145 150 155 160
 Leu His Met Ala Ala Ala Ala Leu Pro His Val Asp Val Thr Lys Pro
 165 170 175
 Gln Gly Val Ile Gly Thr Asn Thr Val Ala Cys Ile Gln Ser Gly Val
 180 185 190
 Tyr Trp Gly Tyr Ile Gly Leu Val Glu Gly Ile Val Arg Gln Ile Arg
 195 200 205
 Met Glu Arg Asp Arg Pro Met Lys Val Ile Ala Thr Gly Gly Leu Ala
 210 215 220
 Ser Leu Phe Asp Leu Gly Phe Asp Leu Phe Asp Lys Val Glu Asp Asp
 225 230 235 240
 Leu Thr Met His Gly Leu Arg Leu Ile Phe Asp Tyr Asn Lys Gly Leu
 245 250 255

Gly Ala

<210> 7

<211> 255

<212> PRT

<213> Geobacter sulfurreducens

<400> 7

Met Leu Leu Val Ile Asp Val Gly Asn Thr Asn Ile Val Leu Gly Ile
 1 5 10 15

Tyr Asp Gly Glu Arg Leu Val Arg Asp Trp Arg Val Ser Thr Asp Lys

20					25					30														
Ala	Arg	Thr	Thr	Asp	Glu	Tyr	Gly	Ile	Leu	Ile	Asn	Glu	Leu	Phe	Arg									
					35					40					45									
Leu	Ala	Gly	Leu	Gly	Leu	Asp	Gln	Ile	Arg	Ala	Val	Ile	Ile	Ser	Ser									
					50					55					60									
Val	Val	Pro	Pro	Leu	Thr	Gly	Val	Leu	Glu	Arg	Leu	Ser	Leu	Gly	Tyr									
					65					70					75					80				
Phe	Gly	Met	Arg	Pro	Leu	Val	Val	Gly	Pro	Gly	Ile	Lys	Thr	Gly	Met									
					85					90					95									
Pro	Ile	Gln	Tyr	Asp	Asn	Pro	Arg	Glu	Val	Gly	Ala	Asp	Arg	Ile	Val									
					100					105					110									
Asn	Ala	Val	Ala	Gly	Tyr	Glu	Lys	Tyr	Arg	Thr	Ser	Leu	Ile	Ile	Val									
					115					120					125									
Asp	Phe	Gly	Thr	Ala	Thr	Thr	Phe	Asp	Tyr	Val	Asn	Arg	Lys	Gly	Glu									
					130					135					140									
Tyr	Cys	Gly	Gly	Ala	Ile	Ala	Pro	Gly	Leu	Val	Ile	Ser	Thr	Glu	Ala									
					145					150					155					160				
Leu	Phe	Gln	Arg	Ala	Ser	Lys	Leu	Pro	Arg	Val	Asp	Ile	Ile	Arg	Pro									
					165					170					175									
Ser	Ala	Ile	Ile	Ala	Arg	Asn	Thr	Val	Asn	Ser	Met	Gln	Ala	Gly	Ile									
					180					185					190									
Tyr	Tyr	Gly	Tyr	Val	Gly	Leu	Val	Asp	Glu	Ile	Val	Thr	Arg	Met	Lys									
					195					200					205									
Ala	Glu	Ser	Lys	Asp	Ala	Pro	Arg	Val	Ile	Ala	Thr	Gly	Gly	Leu	Ala									
					210					215					220									
Ser	Leu	Ile	Ala	Pro	Glu	Ser	Lys	Thr	Ile	Glu	Ala	Val	Glu	Glu	Tyr									
					225					230					235					240				
Leu	Thr	Leu	Glu	Gly	Leu	Arg	Ile	Leu	Tyr	Glu	Arg	Asn	Arg	Glu										
					245					250					255									

<210> 8

<211> 262

<212> PRT

<213> Deinococcus radiopugnans

<400> 8

Met	Pro	Ala	Phe	Pro	Leu	Leu	Ala	Val	Asp	Ile	Gly	Asn	Thr	Thr	Thr									
					1					5					10					15				

Val	Leu	Gly	Leu	Ala	Asp	Ala	Ser	Gly	Ala	Leu	Thr	His	Thr	Trp	Arg				
					20					25					30				

Ile Arg Thr Asn Arg Glu Met Leu Pro Asp Asp Leu Ala Leu Gln Leu
 35 40 45

His Gly Leu Phe Thr Leu Ala Gly Ala Pro Ile Pro Arg Ala Ala Val
 50 55 60

Leu Ser Ser Val Ala Pro Pro Val Gly Glu Asn Tyr Ala Leu Ala Leu
 65 70 75 80

Lys Arg His Phe Met Ile Asp Ala Phe Ala Val Ser Ala Glu Asn Leu
 85 90 95

Pro Asp Val Thr Val Glu Leu Asp Thr Pro Gly Ser Val Gly Ala Asp
 100 105 110

Arg Leu Cys Asn Leu Phe Gly Ala Glu Lys Tyr Leu Gly Gly Leu Asp
 115 120 125

Tyr Ala Val Val Val Asp Phe Gly Thr Ser Thr Asn Phe Asp Val Val
 130 135 140

Gly Arg Gly Arg Arg Phe Leu Gly Gly Ile Leu Ala Thr Gly Ala Gln
 145 150 155 160

Val Ser Ala Asp Ala Leu Phe Ala Arg Ala Ala Lys Leu Pro Arg Ile
 165 170 175

Thr Leu Gln Ala Pro Glu Thr Ala Ile Gly Lys Asn Thr Val His Ala
 180 185 190

Leu Gln Ser Gly Leu Val Phe Gly Tyr Ala Glu Met Val Asp Gly Leu
 195 200 205

Leu Arg Arg Ile Arg Ala Glu Leu Pro Gly Glu Ala Val Ala Val Ala
 210 215 220

Thr Gly Gly Phe Ser Arg Thr Val Gln Gly Ile Cys Gln Glu Ile Asp
 225 230 235 240

Tyr Tyr Asp Glu Thr Leu Thr Leu Arg Gly Leu Val Glu Leu Trp Ala
 245 250 255

Ser Arg Ser Glu Val Arg
 260

<210> 9

<211> 246

<212> PRT

<213> Thermotoga maritima

<400> 9

Met Tyr Leu Leu Val Asp Val Gly Asn Thr His Ser Val Phe Ser Ile
 1 5 10 15

Thr Glu Asp Gly Lys Thr Phe Arg Arg Trp Arg Leu Ser Thr Gly Val
 20 25 30
 Phe Gln Thr Glu Asp Glu Leu Phe Ser His Leu His Pro Leu Leu Gly
 35 40 45
 Asp Ala Met Arg Glu Ile Lys Gly Ile Gly Val Ala Ser Val Val Pro
 50 55 60
 Thr Gln Asn Thr Val Ile Glu Arg Phe Ser Gln Lys Tyr Phe His Ile
 65 70 75 80
 Ser Pro Ile Trp Val Lys Ala Lys Asn Gly Cys Val Lys Trp Asn Val
 85 90 95
 Lys Asn Pro Ser Glu Val Gly Ala Asp Arg Val Ala Asn Val Val Ala
 100 105 110
 Phe Val Lys Glu Tyr Gly Lys Asn Gly Ile Ile Ile Asp Met Gly Thr
 115 120 125
 Ala Thr Thr Val Asp Leu Val Val Asn Gly Ser Tyr Glu Gly Gly Ala
 130 135 140
 Ile Leu Pro Gly Phe Phe Met Met Val His Ser Leu Phe Arg Gly Thr
 145 150 155 160
 Ala Lys Leu Pro Leu Val Glu Val Lys Pro Ala Asp Phe Val Val Gly
 165 170 175
 Lys Asp Thr Glu Glu Asn Ile Arg Leu Gly Val Val Asn Gly Ser Val
 180 185 190
 Tyr Ala Leu Glu Gly Ile Ile Gly Arg Ile Lys Glu Val Tyr Gly Asp
 195 200 205
 Leu Pro Val Val Leu Thr Gly Gly Gln Ser Lys Ile Val Lys Asp Met
 210 215 220
 Ile Lys His Glu Ile Phe Asp Glu Asp Leu Thr Ile Lys Gly Val Tyr
 225 230 235 240
 His Phe Cys Phe Gly Asp
 245

<210> 10
 <211> 273
 <212> PRT
 <213> Treponema pallidum

<400> 10
 Met Leu Leu Ile Asp Val Gly Asn Ser His Val Val Phe Gly Ile Gln
 1 5 10 15

Gly Glu Asn Gly Gly Arg Val Cys Val Arg Glu Leu Phe Arg Leu Ala
 20 25 30

Pro Asp Ala Arg Lys Thr Gln Asp Glu Tyr Ser Leu Leu Ile His Ala
 35 40 45
 Leu Cys Glu Arg Ala Gly Val Gly Arg Ala Ser Leu Arg Asp Ala Phe
 50 55 60
 Ile Ser Ser Val Val Pro Val Leu Thr Lys Thr Ile Ala Asp Ala Val
 65 70 75 80
 Ala Gln Ile Ser Gly Val Gln Pro Val Val Phe Gly Pro Trp Ala Tyr
 85 90 95
 Glu His Leu Pro Val Arg Ile Pro Glu Pro Val Arg Ala Glu Ile Gly
 100 105 110
 Thr Asp Leu Val Ala Asn Ala Val Ala Ala Tyr Val His Phe Arg Ser
 115 120 125
 Ala Cys Val Val Val Asp Cys Gly Thr Ala Leu Thr Phe Thr Ala Val
 130 135 140
 Asp Gly Thr Gly Leu Ile Gln Gly Val Ala Ile Ala Pro Gly Leu Arg
 145 150 155 160
 Thr Ala Val Gln Ser Leu His Thr Gly Thr Ala Gln Leu Pro Leu Val
 165 170 175
 Pro Leu Ala Leu Pro Asp Ser Val Leu Gly Lys Asp Thr Thr His Ala
 180 185 190
 Val Gln Ala Gly Val Val Arg Gly Thr Leu Phe Val Ile Arg Ala Met
 195 200 205
 Ile Ala Gln Cys Gln Lys Glu Leu Gly Cys Arg Cys Ala Ala Val Ile
 210 215 220
 Thr Gly Gly Leu Ser Arg Leu Phe Ser Ser Glu Val Asp Phe Pro Pro
 225 230 235 240
 Ile Asp Ala Gln Leu Thr Leu Ser Gly Leu Ala His Ile Ala Arg Leu
 245 250 255
 Val Pro Thr Ser Leu Leu Pro Pro Ala Thr Val Ser Gly Ser Ser Gly
 260 265 270

Asn

<210> 11
 <211> 262
 <212> PRT
 <213> *Borrelia burgdorferi*

<400> 11
 Met Asn Lys Pro Leu Leu Ser Glu Leu Ile Ile Asp Ile Gly Asn Thr
 1 5 10 15

Ser Ile Ala Phe Ala Leu Phe Lys Asp Asn Gln Val Asn Leu Phe Ile
 20 25 30
 Lys Met Lys Thr Asn Leu Met Leu Arg Tyr Asp Glu Val Tyr Ser Phe
 35 40 45
 Phe Glu Glu Asn Phe Asp Phe Asn Val Asn Lys Val Phe Ile Ser Ser
 50 55 60
 Val Val Pro Ile Leu Asn Glu Thr Phe Lys Asn Val Ile Phe Ser Phe
 65 70 75 80
 Phe Lys Ile Lys Pro Leu Phe Ile Gly Phe Asp Leu Asn Tyr Asp Leu
 85 90 95
 Thr Phe Asn Pro Tyr Lys Ser Asp Lys Phe Leu Leu Gly Ser Asp Val
 100 105 110
 Phe Ala Asn Leu Val Ala Ala Ile Glu Asn Tyr Ser Phe Glu Asn Val
 115 120 125
 Leu Val Val Asp Leu Gly Thr Ala Cys Thr Ile Phe Ala Val Ser Arg
 130 135 140
 Gln Asp Gly Ile Leu Gly Gly Ile Ile Asn Ser Gly Pro Leu Ile Asn
 145 150 155 160
 Phe Asn Ser Leu Leu Asp Asn Ala Tyr Leu Ile Lys Lys Phe Pro Ile
 165 170 175
 Ser Thr Pro Asn Asn Leu Leu Glu Arg Thr Thr Ser Gly Ser Val Asn
 180 185 190
 Ser Gly Leu Phe Tyr Gln Tyr Lys Tyr Leu Ile Glu Gly Val Tyr Arg
 195 200 205
 Asp Ile Lys Gln Met Tyr Lys Lys Lys Phe Asn Leu Ile Ile Thr Gly
 210 215 220
 Gly Asn Ala Asp Leu Ile Leu Ser Leu Ile Glu Ile Glu Phe Ile Phe
 225 230 235 240
 Asn Ile His Leu Thr Val Glu Gly Val Arg Ile Leu Gly Asn Ser Ile
 245 250 255
 Asp Phe Lys Phe Val Asn
 260

<210> 12
 <211> 229
 <212> PRT
 <213> Aquifex aeolicus

<400> 12
 Met Arg Phe Leu Thr Val Asp Val Gly Asn Ser Ser Val Asp Ile Ala

1	5	10	15
Leu Trp Glu Gly Lys Lys Val Lys Asp Phe Leu Lys Leu Ser His Glu	20	25	30
Glu Phe Leu Lys Glu Glu Phe Pro Lys Leu Lys Ala Leu Gly Ile Ser	35	40	45
Val Lys Gln Ser Phe Ser Glu Lys Val Arg Gly Lys Ile Pro Lys Ile	50	55	60
Lys Phe Leu Lys Lys Glu Asn Phe Pro Ile Gln Val Asp Tyr Lys Thr	65	70	75
Pro Glu Thr Leu Gly Thr Asp Arg Val Ala Leu Ala Tyr Ser Ala Lys	85	90	95
Lys Phe Tyr Gly Lys Asn Val Val Val Ile Ser Ala Gly Thr Ala Leu	100	105	110
Val Ile Asp Leu Val Leu Glu Gly Lys Phe Lys Gly Gly Phe Ile Thr	115	120	125
Leu Gly Leu Gly Lys Lys Leu Lys Ile Leu Ser Asp Leu Ala Glu Gly	130	135	140
Ile Pro Glu Phe Phe Pro Glu Glu Val Glu Ile Phe Leu Gly Arg Ser	145	150	155
Thr Arg Glu Cys Val Leu Gly Gly Ala Tyr Arg Glu Ser Thr Glu Phe	165	170	175
Ile Lys Ser Thr Leu Lys Leu Trp Arg Lys Val Phe Lys Arg Lys Phe	180	185	190
Lys Val Val Ile Thr Gly Gly Glu Gly Lys Tyr Phe Ser Lys Phe Gly	195	200	205
Ile Tyr Asp Pro Leu Leu Val His Arg Gly Met Arg Asn Leu Leu Tyr	210	215	220
Leu Tyr His Arg Ile	225		

<210> 13

<211> 257

<212> PRT

<213> Synechocystis sp.

<400> 13

Met Glu Thr Ser Lys Pro Gly Cys Gly Leu Ala Leu Asp Asn Asp Lys	1	5	10	15
-----------------------------------------------------------------	---	---	----	----

Gln Lys Pro Trp Leu Gly Leu Met Ile Gly Asn Ser Arg Leu His Trp	20	25	30
-----------------------------------------------------------------	----	----	----

Ala Tyr Cys Ser Gly Asn Ala Pro Leu Gln Thr Trp Val Thr Asp Tyr
 35 40 45
 Asn Pro Lys Ser Ala Gln Leu Pro Val Leu Leu Gly Lys Val Pro Leu
 50 55 60
 Met Leu Ala Ser Val Val Pro Glu Gln Thr Glu Val Trp Arg Val Tyr
 65 70 75 80
 Gln Pro Lys Ile Leu Thr Leu Lys Asn Leu Pro Leu Val Asn Leu Tyr
 85 90 95
 Pro Ser Phe Gly Ile Asp Arg Ala Leu Ala Gly Leu Gly Thr Gly Leu
 100 105 110
 Thr Tyr Gly Phe Pro Cys Leu Val Val Asp Gly Gly Thr Ala Leu Thr
 115 120 125
 Ile Thr Gly Phe Asp Gln Asp Lys Lys Leu Val Gly Gly Ala Ile Leu
 130 135 140
 Pro Gly Leu Gly Leu Gln Leu Ala Thr Leu Gly Asp Arg Leu Ala Ala
 145 150 155 160
 Leu Pro Lys Leu Glu Met Asp Gln Leu Thr Glu Leu Pro Asp Arg Trp
 165 170 175
 Ala Leu Asp Thr Pro Ser Ala Ile Phe Ser Gly Val Val Tyr Gly Val
 180 185 190
 Leu Gly Ala Leu Gln Ser Tyr Leu Gln Asp Trp Gln Lys Leu Phe Pro
 195 200 205
 Gly Ala Ala Met Val Ile Thr Gly Gly Asp Gly Lys Ile Leu His Gly
 210 215 220
 Phe Leu Lys Glu His Ser Pro Asn Leu Ser Val Ala Trp Asp Asp Asn
 225 230 235 240
 Leu Ile Phe Leu Gly Met Ala Ala Ile His His Gly Asp Arg Pro Ile
 245 250 255

Cys

<210> 14
 <211> 223
 <212> PRT
 <213> Helicobacter pylori

<400> 14
 Met Pro Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys
 1 5 10 15
 Asp Ile Gly Asn Thr Arg Ile His Phe Ala Gln Asn Tyr Gln Leu Phe
 20 25 30

Ser Ser Ala Lys Glu Asp Leu Lys Arg Leu Gly Ile Gln Lys Glu Ile
 35 40 45
 Phe Tyr Ile Ser Val Asn Glu Glu Asn Glu Lys Ala Leu Leu Asn Cys
 50 55 60
 Tyr Pro Asn Ala Lys Asn Ile Ala Gly Phe Phe His Leu Glu Thr Asp
 65 70 75 80
 Tyr Val Gly Leu Gly Ile Asp Arg Gln Met Ala Cys Leu Ala Val Asn
 85 90 95
 Asn Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile Asp Leu Ile
 100 105 110
 Lys Glu Gly Lys His Leu Gly Gly Cys Ile Leu Pro Gly Leu Ala Gln
 115 120 125
 Tyr Ile His Ala Tyr Lys Lys Ser Ala Lys Ile Leu Glu Gln Pro Phe
 130 135 140
 Lys Ala Leu Asp Ser Leu Glu Val Leu Pro Lys Ser Thr Arg Asp Ala
 145 150 155 160
 Val Asn Tyr Gly Met Val Leu Ser Val Ile Ala Cys Ile Gln His Leu
 165 170 175
 Ala Lys Asn Gln Lys Ile Tyr Leu Cys Gly Gly Asp Ala Lys Tyr Leu
 180 185 190
 Ser Ala Phe Leu Pro His Ser Val Cys Lys Glu Arg Leu Val Phe Asp
 195 200 205
 Gly Met Glu Ile Ala Leu Lys Lys Ala Gly Ile Leu Glu Cys Lys
 210 215 220

<210> 15

<211> 267

<212> PRT

<213> Bordetella pertussis

<400> 15

Met Ile Ile Leu Ile Asp Ser Gly Asn Ser Arg Leu Lys Val Gly Trp
 1 5 10 15
 Phe Asp Pro Asp Ala Pro Gln Ala Ala Arg Glu Pro Ala Pro Val Ala
 20 25 30
 Phe Asp Asn Leu Asp Leu Asp Ala Leu Gly Arg Trp Leu Ala Thr Leu
 35 40 45
 Pro Arg Arg Pro Gln Arg Ala Leu Gly Val Asn Val Ala Gly Leu Ala
 50 55 60
 Arg Gly Glu Ala Ile Ala Ala Thr Leu Arg Ala Gly Gly Cys Asp Ile
 65 70 75 80

Arg Trp Leu Arg Ala Gln Pro Leu Ala Met Gly Leu Arg Asn Gly Tyr
 85 90 95
 Arg Asn Pro Asp Gln Leu Gly Ala Asp Arg Trp Ala Cys Met Val Gly
 100 105 110
 Val Leu Ala Arg Gln Pro Ser Val His Pro Pro Leu Leu Val Ala Ser
 115 120 125
 Phe Gly Thr Ala Thr Thr Leu Asp Thr Ile Gly Pro Asp Asn Val Phe
 130 135 140
 Pro Gly Gly Leu Ile Leu Pro Gly Pro Ala Met Met Arg Gly Ala Leu
 145 150 155 160
 Ala Tyr Gly Thr Ala His Leu Pro Leu Ala Asp Gly Leu Val Ala Asp
 165 170 175
 Tyr Pro Ile Asp Thr His Gln Ala Ile Ala Ser Gly Ile Ala Ala Ala
 180 185 190
 Gln Ala Gly Ala Ile Val Arg Gln Trp Leu Ala Gly Arg Gln Arg Tyr
 195 200 205
 Gly Gln Ala Pro Glu Ile Tyr Val Ala Gly Gly Gly Trp Pro Glu Val
 210 215 220
 Arg Gln Glu Ala Glu Arg Leu Leu Ala Val Thr Gly Ala Ala Phe Gly
 225 230 235 240
 Ala Thr Pro Gln Pro Thr Tyr Leu Asp Ser Pro Val Leu Asp Gly Leu
 245 250 255
 Ala Ala Leu Ala Ala Gln Gly Ala Pro Thr Ala
 260 265

<210> 16
 <211> 702
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(699)

<400> 16
 ttg tta ctg gtt atc gat gtg ggg aac acc aat act gta ctt ggt gta 48
 Met Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1 5 10 15
 tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg 96
 Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30
 cat aaa aca gaa gat gag ttt ggg atg att ttg cgc tcc tta ttt gat 144

His	Lys	Thr	Glu	Asp	Glu	Phe	Gly	Met	Ile	Leu	Arg	Ser	Leu	Phe	Asp		
		35					40					45					
cac	tcc	ggg	ctt	atg	ttt	gaa	cag	ata	gat	ggc	att	att	att	tcg	tca	192	
His	Ser	Gly	Leu	Met	Phe	Glu	Gln	Ile	Asp	Gly	Ile	Ile	Ile	Ser	Ser		
	50					55				60							
gta	gtg	ccg	cca	atc	atg	ttt	gcg	tta	gaa	aga	atg	tgc	aca	aaa	tac	240	
Val	Val	Pro	Pro	Ile	Met	Phe	Ala	Leu	Glu	Arg	Met	Cys	Thr	Lys	Tyr		
	65				70				75					80			
ttt	cat	atc	gag	cct	caa	att	gtt	ggc	cca	ggc	atg	aaa	acc	ggc	tta	288	
Phe	His	Ile	Glu	Pro	Gln	Ile	Val	Gly	Pro	Gly	Met	Lys	Thr	Gly	Leu		
			85					90						95			
aat	ata	aaa	tat	gac	aat	ccg	aaa	gaa	gta	ggg	gca	gac	aga	atc	gta	336	
Asn	Ile	Lys	Tyr	Asp	Asn	Pro	Lys	Glu	Val	Gly	Ala	Asp	Arg	Ile	Val		
		100					105					110					
aat	gct	gtc	gct	gcg	ata	cac	ttg	tac	ggc	aat	cca	tta	att	gtt	gtc	384	
Asn	Ala	Val	Ala	Ala	Ile	His	Leu	Tyr	Gly	Asn	Pro	Leu	Ile	Val	Val		
	115					120					125						
gat	ttc	gga	acc	gcc	aca	acg	tac	tgc	tat	att	gat	gaa	aac	aaa	caa	432	
Asp	Phe	Gly	Thr	Ala	Thr	Thr	Tyr	Cys	Tyr	Ile	Asp	Glu	Asn	Lys	Gln		
	130					135					140						
tac	atg	ggc	ggg	gcg	att	gcc	cct	ggg	att	aca	att	tcg	aca	gag	gcg	480	
Tyr	Met	Gly	Gly	Ala	Ile	Ala	Pro	Gly	Ile	Thr	Ile	Ser	Thr	Glu	Ala		
	145			150					155					160			
ctt	tac	tcg	cgt	gca	gca	aag	ctt	cct	cgt	atc	gaa	atc	acc	cgg	ccc	528	
Leu	Tyr	Ser	Arg	Ala	Ala	Lys	Leu	Pro	Arg	Ile	Glu	Ile	Thr	Arg	Pro		
			165					170						175			
gac	aat	att	atc	gga	aaa	aac	act	gtt	agc	gcg	atg	caa	tct	gga	att	576	
Asp	Asn	Ile	Ile	Gly	Lys	Asn	Thr	Val	Ser	Ala	Met	Gln	Ser	Gly	Ile		
		180					185					190					
tta	ttt	ggc	tat	gtc	ggc	caa	gtg	gaa	gga	atc	gtt	aag	cga	atg	aaa	624	
Leu	Phe	Gly	Tyr	Val	Gly	Gln	Val	Glu	Gly	Ile	Val	Lys	Arg	Met	Lys		
	195					200					205						
tgg	cag	gca	aaa	cag	gac	cca	agg	tca	ttg	cga	cag	gag	gcc	tgg	cgc	672	
Trp	Gln	Ala	Lys	Gln	Asp	Pro	Arg	Ser	Leu	Arg	Gln	Glu	Ala	Trp	Arg		
	210				215					220							
cgc	tca	ttg	cga	acg	aat	cag	att	gta	tag							702	
Arg	Ser	Leu	Arg	Thr	Asn	Gln	Ile	Val									
	225				230												

<210> 17
 <211> 233
 <212> PRT
 <213> Bacillus subtilis

<400> 17

Met Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
1 5 10 15

Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
20 25 30

His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
35 40 45

His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
50 55 60

Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
65 70 75 80

Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
85 90 95

Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
100 105 110

Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
115 120 125

Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
130 135 140

Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
145 150 155 160

Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
165 170 175

Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
180 185 190

Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
195 200 205

Trp Gln Ala Lys Gln Asp Pro Arg Ser Leu Arg Gln Glu Ala Trp Arg
210 215 220

Arg Ser Leu Arg Thr Asn Gln Ile Val
225 230

<210> 18

<211> 163

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:promoter
sequence

<220>

<221> -35_signal
<222> (113)..(118)

<220>

<221> -10_signal
<222> (136)..(141)

<400> 18
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tacatccaga acaacctctg ctaaaattcc tgaaaaattt tgcaaaaagt tgttgacttt 120
atctacaagg tgtggtataa taatcttaac aacagcagga cgc 163

<210> 19
<211> 194
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
sequence

<220>
<221> -35_signal
<222> (136)..(141)

<220>
<221> -10_signal
<222> (159)..(164)

<400> 19
gctattgacg acagctatgg ttcaactgtcc accaaccaaa actgtgctca gtaccgccaa 60
tattttctccc ttgaggggta caaagaggtg tccctagaag agatccacgc tgtgtaaaaa 120
ttttacaaaa aggtattgac tttccctaca ggggtgtgtaa taatttaatt acaggcgggg 180
gcaaccccg cgt 194

<210> 20
<211> 248
<212> PRT
<213> Pseudomonas aeruginosa

<400> 20
Met Ile Leu Glu Leu Asp Cys Gly Asn Ser Leu Ile Lys Trp Arg Val
1 5 10 15
Ile Glu Gly Ala Ala Arg Ser Val Ala Gly Gly Leu Ala Glu Ser Asp
20 25 30
Asp Ala Leu Val Glu Gln Leu Thr Ser Gln Gln Ala Leu Pro Val Arg
35 40 45
Ala Cys Arg Leu Val Ser Val Arg Ser Glu Gln Glu Thr Ser Gln Leu
50 55 60
Val Ala Arg Leu Glu Gln Leu Phe Pro Val Ser Ala Leu Val Ala Ser

65	70	75	80
Ser Gly Lys Gln Leu Ala Gly Val Arg Asn Gly Tyr Leu Asp Tyr Gln	85	90	95
Arg Leu Gly Leu Asp Arg Trp Leu Ala Leu Val Ala Ala His His Leu	100	105	110
Ala Lys Lys Ala Cys Leu Val Ile Asp Leu Gly Thr Ala Val Thr Ser	115	120	125
Asp Leu Val Ala Ala Asp Gly Val His Leu Gly Gly Tyr Ile Cys Pro	130	135	140
Gly Met Thr Leu Met Arg Ser Gln Leu Arg Thr His Thr Arg Arg Ile	145	150	155
Arg Tyr Asp Asp Ala Glu Ala Arg Arg Ala Leu Ala Ser Leu Gln Pro	165	170	175
Gly Gln Ala Thr Ala Glu Ala Val Glu Arg Gly Cys Leu Leu Met Leu	180	185	190
Arg Gly Phe Val Arg Glu Gln Tyr Ala Met Ala Cys Glu Leu Leu Gly	195	200	205
Pro Asp Cys Glu Ile Phe Leu Thr Gly Gly Asp Ala Glu Leu Val Arg	210	215	220
Asp Glu Leu Ala Gly Ala Arg Ile Met Pro Asp Leu Val Phe Val Gly	225	230	235
Leu Ala Leu Ala Cys Pro Ile Glu	245		

<210> 21

<211> 209

<212> PRT

<213> Campylobacter jejuni

<400> 21

Met Leu Leu Cys Asp Ile Gly Asn Ser Asn Ala Asn Phe Leu Asp Asp	1	5	10	15
Asn Lys Tyr Phe Thr Leu Asn Ile Asp Gln Phe Leu Glu Phe Lys Asn	20	25	30	
Glu Gln Lys Ile Phe Tyr Ile Asn Val Asn Glu His Leu Lys Glu His	35	40	45	
Leu Lys Asn Gln Lys Asn Phe Ile Asn Leu Glu Pro Tyr Phe Leu Phe	50	55	60	
Asp Thr Ile Tyr Gln Gly Leu Gly Ile Asp Arg Ile Ala Ala Cys Tyr	65	70	75	80

Thr Ile Glu Asp Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile
 85 90 95
 Asp Ile Ile Ser Asn Ser Ile His Leu Gly Gly Phe Ile Leu Pro Gly
 100 105 110
 Ile Ala Asn Tyr Lys Lys Ile Tyr Ser His Ile Ser Pro Arg Leu Lys
 115 120 125
 Ser Glu Phe Asn Thr Gln Val Ser Leu Asp Ala Phe Pro Gln Lys Thr
 130 135 140
 Met Asp Ala Leu Ser Tyr Gly Val Phe Lys Gly Ile Tyr Leu Leu Ile
 145 150 155 160
 Lys Asp Ala Ala Gln Asn Lys Lys Leu Tyr Phe Thr Gly Gly Asp Gly
 165 170 175
 Gln Phe Leu Ala Asn Tyr Phe Asp His Ala Ile Tyr Asp Lys Leu Leu
 180 185 190
 Ile Phe Arg Gly Met Lys Lys Ile Ile Lys Glu Asn Pro Asn Leu Leu
 195 200 205

Tyr

<210> 22
 <211> 592
 <212> PRT
 <213> Neisseria meningitidis

<400> 22
 Met Thr Val Leu Lys Pro Ser His Trp Arg Val Leu Ala Glu Leu Ala
 1 5 10 15
 Asp Gly Leu Pro Gln His Val Ser Gln Leu Ala Arg Met Ala Asp Met
 20 25 30
 Lys Pro Gln Gln Leu Asn Gly Phe Trp Gln Gln Met Pro Ala His Ile
 35 40 45
 Arg Gly Leu Leu Arg Gln His Asp Gly Tyr Trp Arg Leu Val Arg Pro
 50 55 60
 Leu Ala Val Phe Asp Ala Glu Gly Leu Arg Glu Leu Gly Glu Arg Ser
 65 70 75 80
 Gly Phe Gln Thr Ala Leu Lys His Glu Cys Ala Ser Ser Asn Asp Glu
 85 90 95
 Ile Leu Glu Leu Ala Arg Ile Ala Pro Asp Lys Ala His Lys Thr Ile
 100 105 110
 Cys Val Thr His Leu Gln Ser Lys Gly Arg Gly Arg Gln Gly Arg Lys
 115 120 125

Trp Ser His Arg Leu Gly Glu Cys Leu Met Phe Ser Phe Gly Trp Val
 130 135 140
 Phe Asp Arg Pro Gln Tyr Glu Leu Gly Ser Leu Ser Pro Val Ala Ala
 145 150 155 160
 Val Ala Cys Arg Arg Ala Leu Ser Arg Leu Gly Leu Lys Thr Gln Ile
 165 170 175
 Lys Trp Pro Asn Asp Leu Val Val Gly Arg Asp Lys Leu Gly Gly Ile
 180 185 190
 Leu Ile Glu Thr Val Arg Thr Gly Gly Lys Thr Val Ala Val Val Gly
 195 200 205
 Ile Gly Ile Asn Phe Val Leu Pro Lys Glu Val Glu Asn Ala Ala Ser
 210 215 220
 Val Gln Ser Leu Phe Gln Thr Ala Ser Arg Arg Gly Asn Ala Asp Ala
 225 230 235 240
 Ala Val Leu Leu Glu Thr Leu Leu Ala Glu Leu Asp Ala Val Leu Leu
 245 250 255
 Gln Tyr Ala Arg Asp Gly Phe Ala Pro Phe Val Ala Glu Tyr Gln Ala
 260 265 270
 Ala Asn Arg Asp His Gly Lys Ala Val Leu Leu Leu Arg Asp Gly Glu
 275 280 285
 Thr Val Phe Glu Gly Thr Val Lys Gly Val Asp Gly Gln Gly Val Leu
 290 295 300
 His Leu Glu Thr Ala Glu Gly Lys Gln Thr Val Val Ser Gly Glu Ile
 305 310 315 320
 Ser Leu Arg Ser Asp Asp Arg Pro Val Ser Val Pro Lys Arg Arg Asp
 325 330 335
 Ser Glu Arg Phe Leu Leu Leu Asp Gly Gly Asn Ser Arg Leu Lys Trp
 340 345 350
 Ala Trp Val Glu Asn Gly Thr Phe Ala Thr Val Gly Ser Ala Pro Tyr
 355 360 365
 Arg Asp Leu Ser Pro Leu Gly Ala Glu Trp Ala Glu Lys Val Asp Gly
 370 375 380
 Asn Val Arg Ile Val Gly Cys Ala Val Cys Gly Glu Phe Lys Lys Ala
 385 390 395 400
 Gln Val Gln Glu Gln Leu Ala Arg Lys Ile Glu Trp Leu Pro Ser Ser
 405 410 415
 Ala Gln Ala Leu Gly Ile Arg Asn His Tyr Arg His Pro Glu Glu His
 420 425 430

Gly Ser Asp Arg Trp Phe Asn Ala Leu Gly Ser Arg Arg Phe Ser Arg
 435 440 445
 Asn Ala Cys Val Val Val Ser Cys Gly Thr Ala Val Thr Val Asp Ala
 450 455 460
 Leu Thr Asp Asp Gly His Tyr Leu Gly Gly Thr Ile Met Pro Gly Phe
 465 470 475 480
 His Leu Met Lys Glu Ser Leu Ala Val Arg Thr Ala Asn Leu Asn Arg
 485 490 495
 His Ala Gly Lys Arg Tyr Pro Phe Pro Thr Thr Thr Gly Asn Ala Val
 500 505 510
 Ala Ser Gly Met Met Asp Ala Val Cys Gly Ser Val Met Met Met His
 515 520 525
 Gly Arg Leu Lys Glu Lys Thr Gly Ala Gly Lys Pro Val Asp Val Ile
 530 535 540
 Ile Thr Gly Gly Gly Ala Ala Lys Val Ala Glu Ala Leu Pro Pro Ala
 545 550 555 560
 Phe Leu Ala Glu Asn Thr Val Arg Val Ala Asp Asn Leu Val Ile His
 565 570 575
 Gly Leu Leu Asn Leu Ile Ala Ala Glu Gly Gly Glu Ser Glu His Thr
 580 585 590

<210> 23
 <211> 753
 <212> DNA
 <213> Clostridium acetobutylicum

<400> 23
 aataagagag cagcttttat gctgctctta tttttaagga gtgtattaaa agtgatttta 60
 gttttagatg ttggcaatac taatatagtg ttaggaatat acaatgatac gaaacttaca 120
 gctgaatgga gactatcaac agatgtatta agatctgctg acgaatatgg aattcaagta 180
 atgaacttat ttcaacaaga taagctcgat ccaacattag ttgaggaggat aataatatcc 240
 tctgttgtag ctaatatcat gtattcttta gaacatatga taagaaagta ctttaagata 300
 aatccattag ttgttggacc tggaataaaa acaggaatta atattaaata cgataatcct 360
 aaagaagttg gagccgacag aattgtaaat gctgtagcag cacatgaaat ttataaaaaga 420
 tctcttataa taatagattt tggaacagca actacatttt gtgcagtaag agaaaatgga 480
 gattatcttg gtggagcaat atgccctgga attaaagttt catcagaggc tctttttgaa 540
 aaggcagcta agcttccaag agtagagctc ataaaaccag cgtatgctat ttgtaaaaat 600
 actatttcaa gtataacaatc tggaattgtt tatcgatacc tacgtcagggt aaaataactta 660
 tttgaaaaat tgaaagaaaa cctgccggac ggaaggagaa caaggacctc cttggtattg 720
 gccacaggtg gtcttgccaa acttattaat tga 753

<210> 24
 <211> 798
 <212> DNA

<213> *Streptomyces coelicolor*

<400> 24

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atgctgctga cgatcgacgt aggggaacacg cacaccgtcc tcggcctctt cgacggcgag 60
gacatcgctg agcactggcg catctccacg gactcgcgcc gcacggccga cgaactggcg 120
gtgctcctcc agggcctcat gggcatgcat cccctcctcg gcgacgaact gggcgacggc 180
atcgacggca tcgccatctg cgcgacggtc ccctcgtcc tccacgaact gcgcgaggtc 240
acccgccgct actacggcga cgtccccgcg gtcctcgtcg aaccggggcg caagaccggc 300
gtcccgatcc tcaccgacca cccaaggag gtcggcgccg accgcatcat caacgcggta 360
gcggccgtgg agctctacgg cggcccggcg atcgtcgtgg acttcggcac ggcgacgacg 420
ttcgacgcgg tcagcgcgcg cggggagtag atcggcgggc tcatcgcccc cggcatcgag 480
atctcggtcg aggcgtggg cgtcaagggc gccagctcc gcaagatcga ggtggcgcg 540
ccccgcagcg tgatcgga caaacacggc gaggcgatgc agtcgggcat cgtgtacggc 600
ttcgccggcc aggtcgacgg cgtcgtcaac cgcattggcg gggagctggc cgacgacccg 660
gacgacgtga cggatcatgc gacggggcgg ctggcgccga tggtcctggg cgagtcctcg 720
gtcatcgacg agcacgagcc gtgggtgacg ctgatgggtc tgcgcctggg gtacgagcgc 780
aacgtgtcgc gcatgtag                                     798
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<210> 25

<211> 819

<212> DNA

<213> *Mycobacterium tuberculosis*

<400> 25

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gtgctgctgg cgattgacgt ccgcaacacc cacaccgttg tgggcctgct gtccggaatg 60
aaagagcacg caaaggctcg gcagcagtgg cggatacgca ccgaatccga agtcaccgcc 120
gacgaactgg cactgacgat cgacgggctg atcggcgagg attccgagcg gtcaccgggt 180
accgcgcctt tgtccacggt cccgtccgtg ctgcacgagg tgcggataat gtcgaccag 240
tactggccgt cgggtgccga cgtgctgac gagcccggag tacgcaccgg gatccctttg 300
ctcgtcgaca accggaagga agtgggcgca gaccgcatcg tgaactgttt ggccgcctat 360
gaccggttcc ggaaggccgc catcgtcgtt gactttgat cctcgatctg tgttgatgtt 420
gtatcggccca aggttgaatt tcttggcggc gccatcgcg cgggggtgca ggtgtcttcc 480
gatgccgcgg cggcccgtc ggccgcatg cgcgcggtt aacttgccc cccacgttcg 540
gtggttggca agaacaccgt cgaatgcat caagccggtg cgggtgttcg cttcgccggg 600
ctggtagacg ggttggtagg ccgcatccgc gaggacgtgt ccggtttct cgtcgaccac 660
gatgtcgca tcgtggctac cgggcatacc gcgcccctgc tgctgccgga attgcacacc 720
gtcgaccatt acgaccagca cctgacctg cagggctctg ggctggtgtt cgagcgtaac 780
ctcgaagtcc agcgcggccg gctcaagacg gcgcgctga                                     819
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<210> 26

<211> 777

<212> DNA

<213> *Rhodobacter capsulatus*

<400> 26

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atgcttttgt gcatcgactg cggcaacacc aacaccgtgt tttcggctctg ggacgggacg 60
gatttcgccg ccacctggcg catcgccacc gatcatcgcc gcaccgccga cgaatatattc 120
gtctggctga acacgtgat gcaactgaag ggctgcagg gccggatctc cgaggcgatc 180
atctcctcga ccgcgcgcg ggtggtgttc aacctgcgcg ttctgtgcaa ccgctatttc 240
gactgccgcc cctatgtcgt cggcaaaccg ggctgcgagc tgccggtggc gccgcgcgtc 300
gatccgggca ccacggtcgg gccggaccgg ctggtcaata cgggtggcgg ctatgaccgt 360
catggcgggc atctgatcgt cgtcgatttc ggcaccgcca ccaccttga cgtggtggcc 420
cccgatggcg cctatatcgg cggggtgatc gcgcccgggg tgaacctgag ccttgaggcg 480
ctgcatatgg cggcgccgc gctgccgat gtcgacgtca cgaaaccgca aggggtgatc 540
ggcacgaata cgggtggcctg catccaatcc ggggtgtatt ggggctatat cggccttgtc 600
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gaaggcatcg tgcggcagat ccggatggaa cgtgaccgtc cgatgaaggt gattgccacc 660
 ggggtcttg cctcgctctt cgatctgggt ttcgatctgt tcgacaaggt cgaggatgac 720
 ctgaccatgc atggtctgcg tctgatcttc gattacaaca agggacttgg ggcgtga 777

<210> 27

<211> 768

<212> DNA

<213> *Geobacter sulfurreducens*

<400> 27

gtgcttcttg ttatagacgt gggtaataacc aatatcgtgc tcgggattta cgatggcgag 60
 cgcctggtga gggattggcg ggtctccacg gacaaggccc gtactaccga cgagtacggg 120
 attctcataa atgagttggt ccgcttggtg ggccttggtg tcgatcagat ccgcgcggtg 180
 atcatctcct cgggtgtgac gccctcacc ggcgtgctgg agcgtcttc cctggggtat 240
 ttcgggatgc gtccctggt ggtgggaccg ggcataaga caggcatgcc aatccagtac 300
 gacaaccccc gggaggtggg ggccgaccg atcgtgaacg cgggtggcggg gtacgagaag 360
 taccgcacct ctctcattat cgtcgatttc ggcaccgcta ccacgttcga ctacgtgaac 420
 cgcaaggag agtactgcg aggggccatc gcgcgggac tcgtcatttc caccgaggcc 480
 ctgttccagc gggccagcaa gctgccagc gttgatata tacgtccgtc cgcgatcatt 540
 gccaggaaca cggtaattc gatgcaggcg ggaatttact atggttacgt ggggctcgta 600
 gacgagatcg tcaccgggat gaaggccgag agcaaggatg cgccccgggt tatcgctacc 660
 ggagggttgg cgtccctcat agcgccggag tccaagacca tcgaagccgt cgaggaatat 720
 ctgacactgg agggattgcg catactgtac gaacgaaaca gggagtga 768

<210> 28

<211> 789

<212> DNA

<213> *Deinococcus radiodurans*

<400> 28

gtgcccgtt ttccctgct cgccgtggac atcggaaca ccaccaccgt cctgggtctg 60
 gccgacgct cgggcgcct gacccacacc tggcggtatc ggaccaaccg cgagatgctg 120
 cccgacgacc tcgcgtgca actgcacggg ctctttacc tcgccggggc gccgattccc 180
 cgcgcgcgg tgctgagcag cgtggcgccc ccggtgggag aaaactacgc gctcgcgctc 240
 aagcggcact tcatgatcga cgcttttgcc gtgagtgcg agaacctgcc cgacgtgacg 300
 gtggaactcg acacgccggg ctcggtgggt ggcgaccgcc tgtgcaacct ctccggcgcc 360
 gaaaagtacc tgggggggct ggactacgag gtggtagtgg atttcgggac ctccaccaac 420
 tttgacgtgg tggggcgggg gcggcgtttc ctccggcgca tcctcgccac cggagcgacg 480
 gtcagcgccg acgcccgtgt cgcccgcgcc gccaaactgc cgcgcacac cctgcaagcg 540
 cccgagacgg ccacggcaa aaacaccgtc cagcgctgc aatcgggcct ggtcttcggc 600
 tacgccgaga tgggtgacgg cctgctgcgc cgcacccgag ccgagttgcc gggcgaagcg 660
 gtcgccgtcg cactggcggt cttctcgcgc accgtgcagg ggatttgcca ggaaatcgac 720
 tactacgacg aaacgctgac gttgcgcggg ttggtggagc tgtgggcgag ccgttcggag 780
 gtccgctga 789

<210> 29

<211> 741

<212> DNA

<213> *Thermotoga maritima*

<400> 29

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 aaaactttca gaagggtgag gctgtccacc ggtgtgtttc agacggaaga cgaactcttt 120
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<210> 30
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 <212> DNA
 <213> *Treponema pallidum*

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gcagcgggtg	taacgggggg gctttcgcgt cttttctcgt cagagggtga ctttcctcct 720
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<210> 31
 <211> 789
 <212> DNA
 <213> *Borrelia burgdorferi*

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tatttaatag	aagggtgtta tcgtgatatt aagcagatgt ataaaaaaa atttaattta 660	
ataattactg	ggggtaatgc ggacctaat ttgtcattaa ttgagataga gtttattttt 720	
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gttaattga		789

<210> 32

<211> 690
 <212> DNA
 <213> Aquifex aeolicus

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 aagaatgttg tagtaatcag tgcgggtact gcccttgtaa ttgacctagt tcttgagggc 360
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<210> 33
 <211> 774
 <212> DNA
 <213> Synechocystis sp.

<400> 33
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 atattacatg gcttcctaaa agagcattct cctaattctt cgggtggcctg ggatgacaat 720
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<210> 34
 <211> 672
 <212> DNA
 <213> Helicobacter pylori

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<210> 35

<211> 747

<212> DNA

<213> *Pseudomonas aeruginosa*

<400> 35

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<210> 36

<211> 630

<212> DNA

<213> *Campylobacter jejuni*

<400> 36

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<210> 37

<211> 1779

<212> DNA

<213> *Neisseria meningitidis*

<400> 37

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<210> 38
 <211> 804
 <212> DNA
 <213> Bordetella pertussis

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<400> 38
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<210> 39
 <211> 460
 <212> PRT
 <213> Neisseria gonorrhoeae

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<400> 39
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Gln Tyr Glu Leu Gly Ser Leu Ser Pro Val Ala Ala Leu Ala Cys Arg
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Arg Ala Leu Gly Cys Leu Gly Leu Glu Thr Gln Ile Lys Trp Pro Asn
 35 40 45
 Asp Leu Val Val Gly Arg Asp Lys Leu Gly Gly Ile Leu Ile Glu Thr
 50 55 60
 Val Arg Ala Gly Gly Lys Thr Val Ala Val Val Gly Ile Gly Ile Asn
 65 70 75 80
 Phe Val Leu Pro Lys Glu Val Glu Asn Ala Ala Ser Val Gln Ser Leu
 85 90 95
 Phe Gln Thr Ala Ser Arg Arg Gly Asn Ala Asp Ala Ala Val Leu Leu
 100 105 110
 Glu Thr Leu Leu Ala Glu Leu Gly Ala Val Leu Glu Gln Tyr Ala Glu
 115 120 125
 Glu Gly Phe Ala Pro Phe Leu Asn Glu Tyr Glu Thr Ala Asn Arg Asp
 130 135 140
 His Gly Lys Ala Val Leu Leu Arg Asp Gly Glu Thr Val Cys Glu
 145 150 155 160
 Gly Thr Val Lys Gly Val Asp Gly Arg Gly Val Leu His Leu Glu Thr
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 Ala Glu Gly Glu Gln Thr Val Val Ser Gly Glu Ile Ser Leu Arg Pro
 180 185 190
 Asp Asn Arg Ser Val Ser Val Pro Lys Arg Pro Asp Ser Glu Arg Phe
 195 200 205
 Leu Leu Leu Glu Gly Gly Asn Ser Arg Leu Lys Trp Ala Trp Val Glu
 210 215 220
 Asn Gly Thr Phe Ala Thr Val Gly Ser Ala Pro Tyr Arg Asp Leu Ser
 225 230 235 240
 Pro Leu Gly Ala Glu Trp Ala Glu Lys Ala Asp Gly Asn Val Arg Ile
 245 250 255
 Val Gly Cys Ala Val Cys Gly Glu Ser Lys Lys Ala Gln Val Lys Glu
 260 265 270
 Gln Leu Ala Arg Lys Ile Glu Trp Leu Pro Ser Ser Ala Gln Ala Leu
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 Gly Ile Arg Asn His Tyr Arg His Pro Glu Glu His Gly Ser Asp Arg
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 Trp Phe Asn Ala Leu Gly Ser Arg Arg Phe Ser Arg Asn Ala Cys Val
 305 310 315 320
 Val Val Ser Cys Gly Thr Ala Val Thr Val Asp Ala Leu Thr Asp Asp
 325 330 335

Gly His Tyr Leu Gly Gly Thr Ile Met Pro Gly Phe His Leu Met Lys
 340 345 350
 Glu Ser Leu Ala Val Arg Thr Ala Asn Leu Asn Arg Pro Ala Gly Lys
 355 360 365
 Arg Tyr Pro Phe Pro Thr Thr Thr Gly Asn Ala Val Ala Ser Gly Met
 370 375 380
 Met Asp Ala Val Cys Gly Ser Ile Met Met Met His Gly Arg Leu Lys
 385 390 395 400
 Glu Lys Asn Gly Ala Gly Lys Pro Val Asp Val Ile Ile Thr Gly Gly
 405 410 415
 Gly Ala Ala Lys Val Ala Glu Ala Leu Pro Pro Ala Phe Leu Ala Glu
 420 425 430
 Asn Thr Val Arg Val Ala Asp Asn Leu Val Ile His Gly Leu Leu Asn
 435 440 445
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<210> 40
 <211> 1383
 <212> DNA
 <213> Neisseria gonorrhoeae

<400> 40

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<210> 41
 <211> 244
 <212> PRT
 <213> Porphyromonas gingivalis

<400> 41

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Lys	Ala	Gly	Gln	Ala	Leu	Ser	His	Leu	Val	Ala	Pro	His	Arg	Phe	Asp
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Pro	Val	Pro	Leu	Arg	Leu	Gln	Tyr	Asp	Arg	Arg	Thr	Leu	Gly	Ala	Asp
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Pro	Ser	Gly	Ile	Ser	Pro	Lys	Ile	Ala	Glu	Tyr	Gly	Ser	Ser	Thr	Glu
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		210				215					220				
Ile	Leu	Ile	His	Pro	Asp	Leu	Val	Leu	Leu	Gly	Leu	Asn	Arg	Ile	Leu
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Glu	Tyr	Asn	Val												

<210> 42

<211> 735
 <212> DNA
 <213> Porphyromonas gingivalis

<400> 42
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 ctcgtcgctc ctcaccggtt cgacaaggct atctactcat ctgtggggct tcccgcagaa 180
 gaggtgaag ctattgtgag aagttgtgca gctgcttctt tgatgatggg gactgagacc 240
 cccgtacccc ttcgcctgca atatgatcgc cgcacttttg gtgccgaccg actgggtgcg 300
 gtggtcggag cgcatagtct ctatccgaat accgaattgc tggatgatcga cgccgggtact 360
 gccatcactt atgaacgagt atccgctgaa gggatctatc tcgggtggcaa tatatcgccc 420
 ggtctccact tgcgcttcaa ggctcttcat ctctttacgg gcaggctccc cctgattgat 480
 ccttccggta tctctccgaa aatagccgag tatggctcct cgaccgaaga agcgatcaca 540
 gccggagtaa ttcattggcct ggcaggggag atagacagat atattgacga tctgcacgct 600
 aaagaggggc ggtctgccgt tatactgacc ggaggagatg ccaactattt ggcacggatt 660
 ataagaagcg gaataactaat tcatcccgat ttagtacttt tgggcctaaa tagaatttta 720
 gaatataatg tataa 735

<210> 43
 <211> 592
 <212> PRT
 <213> Neisseria meningitidis

<400> 43
 Met Thr Val Leu Lys Leu Ser His Trp Arg Val Leu Ala Glu Leu Ala
 1 5 10 15
 Asp Gly Leu Pro Gln His Val Ser Gln Leu Ala Arg Met Ala Asp Met
 20 25 30
 Lys Pro Gln Gln Leu Asn Gly Phe Trp Gln Gln Met Pro Ala His Ile
 35 40 45
 Arg Gly Leu Leu Arg Gln His Asp Gly Tyr Trp Arg Leu Val Arg Pro
 50 55 60
 Leu Ala Val Phe Asp Ala Glu Gly Leu Arg Glu Leu Gly Glu Arg Ser
 65 70 75 80
 Gly Phe Gln Thr Ala Leu Lys His Glu Cys Ala Ser Ser Asn Asp Glu
 85 90 95
 Ile Leu Glu Leu Ala Arg Ile Ala Pro Asp Lys Ala His Lys Thr Ile
 100 105 110
 Cys Val Thr His Leu Gln Ser Lys Gly Arg Gly Arg Gln Gly Arg Lys
 115 120 125
 Trp Ser His Arg Leu Gly Glu Cys Leu Met Phe Ser Phe Gly Trp Val
 130 135 140
 Phe Asp Arg Pro Gln Tyr Glu Leu Gly Ser Leu Ser Pro Val Ala Ala
 145 150 155 160

Val Ala Cys Arg Arg Ala Leu Ser Arg Leu Gly Leu Asp Val Gln Ile
165 170 175
Lys Trp Pro Asn Asp Leu Val Val Gly Arg Asp Lys Leu Gly Gly Ile
180 185 190
Leu Ile Glu Thr Val Arg Thr Gly Gly Lys Thr Val Ala Val Val Gly
195 200 205
Ile Gly Ile Asn Phe Val Leu Pro Lys Glu Val Glu Asn Ala Ala Ser
210 215 220
Val Gln Ser Leu Phe Gln Thr Ala Ser Arg Arg Gly Asn Ala Asp Ala
225 230 235 240
Ala Val Leu Leu Glu Thr Leu Leu Val Glu Leu Asp Ala Val Leu Leu
245 250 255
Gln Tyr Ala Arg Asp Gly Phe Ala Pro Phe Val Ala Glu Tyr Gln Ala
260 265 270
Ala Asn Arg Asp His Gly Lys Ala Val Leu Leu Leu Arg Asp Gly Glu
275 280 285
Thr Val Phe Glu Gly Thr Val Lys Gly Val Asp Gly Gln Gly Val Leu
290 295 300
His Leu Glu Thr Ala Glu Gly Lys Gln Thr Val Val Ser Gly Glu Ile
305 310 315 320
Ser Leu Arg Ser Asp Asp Arg Pro Val Ser Val Pro Lys Arg Arg Asp
325 330 335
Ser Glu Arg Phe Leu Leu Leu Asp Gly Gly Asn Ser Arg Leu Lys Trp
340 345 350
Ala Trp Val Glu Asn Gly Thr Phe Ala Thr Val Gly Ser Ala Pro Tyr
355 360 365
Arg Asp Leu Ser Pro Leu Gly Ala Glu Trp Ala Glu Lys Ala Asp Gly
370 375 380
Asn Val Arg Ile Val Gly Cys Ala Val Cys Gly Glu Phe Lys Lys Ala
385 390 395 400
Gln Val Gln Glu Gln Leu Ala Arg Lys Ile Glu Trp Leu Pro Ser Ser
405 410 415
Ala Gln Ala Leu Gly Ile Arg Asn His Tyr Arg His Pro Glu Glu His
420 425 430
Gly Ser Asp Arg Trp Phe Asn Ala Leu Gly Ser Arg Arg Phe Ser Arg
435 440 445
Asn Ala Cys Val Val Val Ser Cys Gly Thr Ala Val Thr Val Asp Ala
450 455 460

Leu Thr Asp Asp Gly His Tyr Leu Gly Gly Thr Ile Met Pro Gly Phe
 465 470 475 480
 His Leu Met Lys Glu Ser Leu Ala Val Arg Thr Ala Asn Leu Asn Arg
 485 490 495
 His Ala Gly Lys Arg Tyr Pro Phe Pro Thr Thr Thr Gly Asn Ala Val
 500 505 510
 Ala Ser Gly Met Met Asp Ala Val Cys Gly Ser Val Met Met Met His
 515 520 525
 Gly Arg Leu Lys Glu Lys Thr Gly Ala Gly Lys Pro Val Asp Val Ile
 530 535 540
 Ile Thr Gly Gly Gly Ala Ala Lys Val Ala Glu Ala Leu Pro Pro Ala
 545 550 555 560
 Phe Leu Ala Glu Asn Thr Val Arg Val Ala Asp Asn Leu Val Ile Tyr
 565 570 575
 Gly Leu Leu Asn Met Ile Ala Ala Glu Gly Arg Glu Tyr Glu His Ile
 580 585 590

<210> 44

<211> 1779

<212> DNA

<213> Neisseria meningitidis

<400> 44

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 caacacgtct cgcaactggc gcgtatggcg gatatgaagc cgcagcagct caacggtttt 120
 tggcagcaga tgccggcgca ctaacgcggg ctggttgcgc aacacgacgg ctattggcgg 180
 ctggtgcgcc cattggcggg ttctgatgcc gaaggtttgc gcgagctggg ggaaaggctc 240
 ggttttcaga cggcattgaa gcacgagtcg gcgtccagca acgacgagat actggaattg 300
 gcgcggattg cgccggacaa ggcgcacaaa accatatgcg tgaccacact gcaaagtaag 360
 ggcagggggc ggcagggggc gaagtggcgg caccgtttgg gcgagtgtct gatgttcagt 420
 tttggctggg tgtttgaccg gccgcagtat gagttgggtt cgctgtcgcc tgttgcggca 480
 gtggcgtgtc ggcgcgcctt gtgcgcttta ggtttggatg tgcagattaa gtggcccaat 540
 gatttggttg tcggacgcga caaattgggc ggcattctga ttgaaacggt caggacgggc 600
 ggcaaaacgg ttgccgtggg cggatcggc atcaattttg tcctgcccga ggaagtagaa 660
 aatgccgctt ccgtgcaatc gctgtttcag acggcatcgc ggcggggcaa tgccgatgcc 720
 gccgtgctgc tggaaacgct gttggtggaa ctggacgcgg tgttgttgca atatgcgcgg 780
 gacggatttg cgccttttgt ggcggaatat caggctgcca accgcgacca cggcaaggcg 840
 gtattgctgt tgcgcgacgg cgaaaccgtg ttcgaaggca cggttaaagg cgtggacgga 900
 caaggcggtt tgcacttgga aacggcagag ggcaaacaga cggtcgtcag cggcgaaatc 960
 agcctgcggt ccgacgacag gccggtttcc gtgccgaagc ggcgggattc ggaacgtttt 1020
 ctgctgttgg acggcggaac cagccggctc aagtgggctg ggtggaaaaa cggcacgttc 1080
 gcaaccgtcg gtagcgcgcc gtaccgcgat ttgtcgctt tgggcgcgga gtgggcggaa 1140
 aaggcggatg gaaatgtccg catcgtcggt tgcgctgtgt gcggagaatt caaaaaggca 1200
 caagtgcagg aacagctcgc ccgaaaaatc gagtggctgc cgtcttccgc acaggctttg 1260
 ggcatacgca accactaccg ccaccccga gaacacggtt ccgaccgctg gttcaacgcc 1320
 ttgggcagcc gccgcttcag ccgcaacgcc tgcgtcgtcg tcagttgcgg cagggcggtg 1380
 acggttgacg cgctcaccga tgacggacat tatctcgggg gaaccatcat gcccggtttc 1440
 cacctgatga aagaatcgct cgccgtccga accgccaacc tcaaccggca cgcgggtaag 1500
 cgttatcctt tcccgaccac aacgggcaat gccgtcgcca gcggcatgat ggatgcgggt 1560

tgcggctcgg ttatgatgat gcacgggctg ttgaaagaaa aaaccggggc gggcaagcct 1620
 gtcgatgtca tcattaccgg cggcggcgcg gcaaaagtgg ccgaagccct gccgcctgca 1680
 tttttggcgg aaaataccgt gcgcgtggcg gacaacctcg tcatttacgg gttgttgaac 1740
 atgattgccg ccgaaggcag ggaatatgaa catatttaa 1779

<210> 45
 <211> 262
 <212> PRT
 <213> *Bacillus anthracis*

<400> 45

Met	Ile	Phe	Val	Leu	Asp	Val	Gly	Asn	Thr	Asn	Ala	Val	Leu	Gly	Val	1	5	10	15
Phe	Glu	Glu	Gly	Glu	Leu	Arg	Gln	His	Trp	Arg	Met	Glu	Thr	Asp	Arg	20	25	30	
His	Lys	Thr	Glu	Asp	Glu	Tyr	Gly	Met	Leu	Val	Lys	Gln	Leu	Leu	Glu	35	40	45	
His	Glu	Gly	Leu	Ser	Phe	Glu	Asp	Val	Lys	Gly	Ile	Ile	Val	Ser	Ser	50	55	60	
Val	Val	Pro	Pro	Ile	Met	Phe	Ala	Leu	Glu	Arg	Met	Cys	Glu	Lys	Tyr	65	70	75	80
Phe	Lys	Ile	Lys	Pro	Leu	Val	Val	Gly	Pro	Gly	Ile	Lys	Thr	Gly	Leu	85	90	95	
Asn	Ile	Lys	Tyr	Glu	Asn	Pro	Arg	Glu	Val	Gly	Ala	Asp	Arg	Ile	Val	100	105	110	
Asn	Ala	Val	Ala	Gly	Ile	His	Leu	Tyr	Gly	Ser	Pro	Leu	Ile	Ile	Val	115	120	125	
Asp	Phe	Gly	Thr	Ala	Thr	Thr	Tyr	Cys	Tyr	Ile	Asn	Glu	Glu	Lys	His	130	135	140	
Tyr	Met	Gly	Gly	Val	Ile	Thr	Pro	Gly	Ile	Met	Ile	Ser	Ala	Glu	Ala	145	150	155	160
Leu	Tyr	Ser	Arg	Ala	Ala	Lys	Leu	Pro	Arg	Ile	Glu	Ile	Thr	Lys	Pro	165	170	175	
Ser	Ser	Val	Val	Gly	Lys	Asn	Thr	Val	Ser	Ala	Met	Gln	Ser	Gly	Ile	180	185	190	
Leu	Tyr	Gly	Tyr	Val	Gly	Gln	Val	Glu	Gly	Ile	Val	Lys	Arg	Met	Lys	195	200	205	
Glu	Glu	Ala	Lys	Gln	Glu	Pro	Lys	Val	Ile	Ala	Thr	Gly	Gly	Leu	Ala	210	215	220	
Lys	Leu	Ile	Ser	Glu	Glu	Ser	Asn	Val	Ile	Asp	Val	Val	Asp	Pro	Phe	225	230	235	240

Leu Thr Leu Lys Gly Leu Tyr Met Leu Tyr Glu Arg Asn Ala Asn Leu
245 250 255

Gln His Glu Lys Gly Glu
260

<210> 46
<211> 789
<212> DNA
<213> Bacillus anthracis

<400> 46
atgatttttg tattggatgt agggaacaca aatgctgtac tgggcgtggt tgaagagggg 60
gaacttcgtc aacattggcg catggaaaca gatcgtcata agacagaaga tgaatatgga 120
atgcttgatga agcagttgct tgagcatgag ggtctttcgt ttgaagatgt gaaaggtatt 180
atcgatatctt cagtcgtgcc accaattatg tttgcttttag agcgcatgtg tgaaaagtat 240
tttaaaatta agccgcttgt agtaggtcct ggaataaaaa cggggctaaa tattaaatat 300
gaaaatccac gtgaagtagg tgcggatcga atcgtaaag cagtagcagg gatccactta 360
tatggaagtc cgcttattat tgcgattttt ggtacggcta ctacatattg ttatattaac 420
gaagaaaagc attatatggg tggagttatt acaccgggaa ttatgatttc agcagagggt 480
ttatatagta gagccgcaaa acttcctcgt attgaaatta caaaaccaag cagtgtagtt 540
gggaagaata cggtaagtgc gatgcaatct ggtattcttt atggttatgt tggacaagtg 600
gaaggtattg ttaagcgcat gaaagaggaa gctaaacaag aaccgaaagt tattgcaaca 660
ggtggattgg cgaaattaat ttcagaagaa tcgaatgtga ttgatgttgt agatccattt 720
ttaacattaa aaggtttgta tatgtttatc gagcggaatg caaatttaca gcatgagaaa 780
ggtgaataa 789

<210> 47
<211> 254
<212> PRT
<213> Bacillus halodurans

<400> 47
Met Ile Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
1 5 10 15
Tyr Gln Asp Glu Thr Leu Val His His Trp Arg Leu Ala Thr Ser Arg
20 25 30
Gln Lys Thr Glu Asp Glu Tyr Ala Met Thr Val Arg Ser Leu Phe Asp
35 40 45
His Ala Gly Leu Gln Phe Gln Asp Ile Asp Gly Ile Val Ile Ser Ser
50 55 60
Val Val Pro Pro Met Met Phe Ser Leu Glu Gln Met Cys Lys Lys Tyr
65 70 75 80
Phe His Val Thr Pro Met Ile Ile Gly Pro Gly Ile Lys Thr Gly Leu
85 90 95
Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
100 105 110
Asn Ala Val Ala Ala Ile Glu Leu Tyr Gly Tyr Pro Ala Ile Val Val

115 120 125
 Asp Phe Gly Thr Ala Thr Thr Tyr Cys Leu Ile Asn Glu Lys Lys Gln
 130 135 140
 Tyr Ala Gly Gly Val Ile Ala Pro Gly Ile Met Ile Ser Thr Glu Ala
 145 150 155 160
 Leu Tyr His Arg Ala Ser Lys Leu Pro Arg Ile Glu Ile Ala Lys Pro
 165 170 175
 Lys Gln Val Val Gly Thr Asn Thr Ile Asp Ser Met Gln Ser Gly Ile
 180 185 190
 Phe Tyr Gly Tyr Val Ser Gln Val Asp Gly Val Val Lys Arg Met Lys
 195 200 205
 Ala Gln Ala Glu Ser Glu Pro Lys Val Ile Ala Thr Gly Gly Leu Ala
 210 215 220
 Lys Leu Ile Gly Thr Glu Ser Glu Thr Ile Asp Val Ile Asp Ser Phe
 225 230 235 240
 Leu Thr Leu Lys Gly Leu Gln Leu Ile Tyr Lys Lys Asn Val
 245 250

<210> 48
 <211> 765
 <212> DNA
 <213> Bacillus halodurans

<400> 48
 atgatacttg tcattgatgt tggaaataca aatactgtgt taggggtcta ccaagatgaa 60
 acgttagtgc atcattggcg gctagcgacg agtaggcaaa agaccgagga tgagtatgca 120
 atgacggtgc gttctctctt tgatcatgca ggtctacagt ttcaagacat agacggcatt 180
 gtcatttcat ctgttggtccc accgatgatg ttttccttag agcaaattgt caaaaaatac 240
 tttcatgtca ctccatgatg tattgggcct ggaattaaga caggcttaaa tattaagtat 300
 gacaatccaa aagagggttg ggccgatcga atcggttaat cagttgcagc gattgagtta 360
 tatggctacc ctgccattgt cggtgatttt ggaacagcaa caacatattg cttaattaat 420
 gaaaaaaaaa aatatgcagg gggagtcatt gctcctggaa tcatgatctc aacagaagcg 480
 ttgtatcatc gcgcatcaaa attgccacgg attgaaatag cgaagccgaa acaagtcgta 540
 gggacaaata cgattgattc gatgcaatca ggaatcttct acgggtatgt gagccaagtc 600
 gatggtgttg tgaacgaat gaaggctcaa gcagaaaagt aaccgaaaagt cattgcaact 660
 ggtgggcttg cgaagttaat cggaaccgag tcggaacca ttgatgtaat cgattcgttt 720
 ttaacattaa aaggattgca actcatttat aagaagaatg tctga 765

<210> 49
 <211> 258
 <212> PRT
 <213> Bacillus stearothermophilus

<400> 49
 Met Ile Phe Val Leu Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1 5 10 15

Tyr Asp Gly Asp Glu Leu Lys His His Trp Arg Ile Glu Thr Ser Arg
 20 25 30
 Ser Lys Thr Glu Asp Glu Tyr Gly Met Met Ile Lys Ala Leu Leu Asn
 35 40 45
 His Val Gly Leu Gln Phe Ser Asp Ile Arg Gly Ile Ile Ile Ser Ser
 50 55 60
 Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Leu Lys Tyr
 65 70 75 80
 Phe His Ile Lys Pro Leu Ile Val Gly Pro Gly Ile Lys Thr Gly Leu
 85 90 95
 Asp Ile Lys Tyr Asp Asn Pro Arg Glu Val Gly Ala Asp Arg Ile Val
 100 105 110
 Asn Ala Val Ala Gly Ile His Leu Tyr Gly Ser Pro Leu Ile Ile Val
 115 120 125
 Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asn Glu His Lys Gln
 130 135 140
 Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Met Ile Ser Thr Glu Ala
 145 150 155 160
 Leu Phe Ala Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Ala Arg Pro
 165 170 175
 Asp Asp Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ala Gly Ile
 180 185 190
 Leu Tyr Gly Tyr Val Gly Gln Val Glu Gly Ile Val Ser Arg Met Lys
 195 200 205
 Ala Lys Ser Lys Ile Pro Pro Lys Val Ile Ala Thr Gly Gly Leu Ala
 210 215 220
 Pro Leu Ile Ala Ser Glu Ser Asp Ile Ile Asp Val Val Asp Pro Phe
 225 230 235 240
 Leu Thr Leu Thr Gly Leu Lys Leu Leu Tyr Glu Lys Asn Thr Glu Lys
 245 250 255
 Lys Gly

<210> 50
 <211> 777
 <212> DNA
 <213> Bacillus stearothermophilus

<400> 50
 atgatttttg tattggacgt cggcaataca aacacggtgt taggggtgta tgacggggac 60
 gaactgaaac atcattggcg cattgaaaca agccgctcga aaacggaaga cgaatacggc 120

```

atgatgatca aagcgtctctt gaaccatgtc ggcttgacgt tttccgacat tcgaggcatc 180
atcatttcct cggtcgtgcc gccgattatg tttgctcttg aacgcatgtg tctaaaatat 240
ttccatatca aaccgctcat cgtcgggtccg ggcattaaaa ccggggtcga catcaaatat 300
gacaatccgc gtgaggtggg cggcgaccgg attgtcaacg cggttgccgg catccatttg 360
tacggcagtc cgctgattat cgtcgatttt ggcacggcga cgacgtattg ttatattaat 420
gaacataaac aatatatggg aggggccatt gcccgggaa ttatgatctc gacagaggct 480
ctgtttgcgc gggcggcgaa attgccgcgc attgaaatcg cccgcccgga tgatatcatc 540
ggcaaaaata cggtcagcgc catgcaagcc ggtattttat acggttatgt cggacaagtg 600
gaaggcatcg tgtcgcgaat gaaggcgaaa agcaaaatcc cgccgaaggt gattgctact 660
ggcggtttgg ctccgctcat tgccagcgaa tcggacatca tcgatgtcgt tgatccgttt 720
ttgacgctga ctggcttaaa attgttgtac gagaaaaaca ccgagaaaaa aggatga 777

```

<210> 51
 <211> 260
 <212> PRT
 <213> *Caulobacter crescentus*

<400> 51

```

Met Leu Leu Ala Ile Glu Gln Gly Asn Thr Asn Thr Met Phe Ala Ile
  1                      5                      10                      15

```

```

His Asp Gly Ala Ser Trp Val Ala Gln Trp Arg Ser Ala Thr Glu Ser
          20                      25                      30

```

```

Thr Arg Thr Ala Asp Glu Tyr Val Val Trp Leu Ser Gln Leu Leu Ser
      35                      40                      45

```

```

Met Gln Gly Leu Gly Phe Arg Ala Ile Asp Ala Val Ile Ile Ser Ser
  50                      55                      60

```

```

Val Val Pro Gln Ser Ile Phe Asn Leu Arg Asn Leu Ser Arg Arg Tyr
  65                      70                      75                      80

```

```

Phe Asn Val Glu Pro Leu Val Ile Gly Glu Asn Ala Lys Leu Gly Ile
          85                      90                      95

```

```

Asp Val Arg Ile Glu Lys Pro Ser Glu Ala Gly Ala Asp Arg Leu Val
      100                      105                      110

```

```

Asn Ala Ile Gly Ala Ala Met Val Tyr Pro Gly Pro Leu Val Val Ile
      115                      120                      125

```

```

Asp Ser Gly Thr Ala Thr Thr Phe Asp Ile Val Ala Ala Asp Gly Ala
      130                      135                      140

```

```

Phe Glu Gly Gly Ile Ile Ala Pro Gly Ile Asn Leu Ser Met Gln Ala
      145                      150                      155                      160

```

```

Leu His Glu Ala Ala Ala Lys Leu Pro Arg Ile Ala Ile Gln Arg Pro
          165                      170                      175

```

```

Ala Gly Asn Arg Ile Val Gly Thr Asp Thr Val Ser Ala Met Gln Ser
          180                      185                      190

```

```

Gly Val Phe Trp Gly Tyr Ile Ser Leu Ile Glu Gly Leu Val Ala Arg
      195                      200                      205

```


Ile Lys Ala Glu Arg Gly Glu Pro Met Thr Val Ile Ala Thr Gly Gly
 210 215 220

Val Ala Ser Leu Phe Glu Gly Ala Thr Asp Ser Ile Asp His Phe Asp
 225 230 235 240

Ser Asp Leu Thr Ile Arg Gly Leu Leu Glu Ile Tyr Arg Arg Asn Thr
 245 250 255

Ile Ala Glu Ser
 260

<210> 52
 <211> 783
 <212> DNA
 <213> *Caulobacter crescentus*

<400> 52
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 tcgtgggtcg cgcagtggcg gtcagcgacc gaaagcacgc gcacggccga tgagtacgtc 120
 gtctggcttt cgcaactgct gtcgatgcag gggcttggct tccgggcat cgacgccgtg 180
 atcatttcca gcgtcggtgcc gcagtcgac ttcaatctgc gcaacctgag ccgccgctac 240
 ttcaacgtcg agcctctggt catcggtgag aacgccaaagc tgggcattga tgtccgcac 300
 gagaaacctt ccgaggcccg cgccgaccgc ctggtcaacg ccattggcgc ggcgatggc 360
 tatccgggtc cgctggtcgt gatcgacagc ggcaccgcca cgacgttcga catcgtggc 420
 gccgacggcg ccttcgaggg cgggattatc gcgcccggta tcaacctgtc gatgcaggc 480
 ctgcacgagg cggcggcgaa gctgccgcgc atcgccatcc agcgtcccgc cggtaacagg 540
 atcgtgggca cggacacggt ctccgccatg cagtccggcg tcttctgggg ctatatttcg 600
 ctgatcgaag gcctcgtcgc gcggatcaag gccgagcgcg gcgagcctat gaccgttatc 660
 gccacgggtg gcgtcgctc gctgttcgag ggcgcgaccg acagcattga ccacttcgac 720
 tctgatctga cgatccgggg tcttctcgaa atctaccgcc gaaacaccat cgccgagtc 780
 tga 783

<210> 53
 <211> 257
 <212> PRT
 <213> *Chlorobium tepidum*

<400> 53
 Met Arg Leu Val Val Asp Ile Gly Asn Thr Ser Thr Thr Leu Ala Ile
 1 5 10 15

Phe Thr Gly Asp Glu Glu Pro Ser Val Glu Ser Val Pro Ser Ala Leu
 20 25 30

Phe Ala Asp Ser Ser Thr Met Arg Glu Val Phe Gly Asn Met Ala Arg
 35 40 45

Lys His Gly Glu Pro Gln Ala Ile Ala Ile Cys Ser Val Val Pro Ser
 50 55 60

Ala Thr Ala Val Gly Ser Ala Leu Leu Glu Ser Leu Phe Ser Val Pro
 65 70 75 80

Val	Leu	Thr	Ile	Cys	Cys	Lys	Leu	Arg	Phe	Pro	Phe	Arg	Leu	Asp	Tyr	
				85					90					95		
Ala	Thr	Pro	His	Thr	Phe	Gly	Ala	Asp	Arg	Leu	Ala	Leu	Cys	Ala	Trp	
			100					105					110			
Ser	Arg	His	Leu	Phe	Ser	Glu	Lys	Pro	Val	Ile	Ala	Val	Asp	Ile	Gly	
		115					120					125				
Thr	Ala	Ile	Thr	Phe	Asp	Val	Leu	Asp	Thr	Val	Gly	Asn	Tyr	Arg	Gly	
	130					135					140					
Gly	Leu	Ile	Met	Pro	Gly	Ile	Asp	Met	Met	Ala	Gly	Ala	Leu	His	Ser	
145					150					155					160	
Arg	Thr	Ala	Gln	Leu	Pro	Gln	Val	Arg	Ile	Asp	Arg	Pro	Glu	Ser	Leu	
			165					170						175		
Leu	Gly	Arg	Ser	Thr	Thr	Glu	Cys	Ile	Lys	Ser	Gly	Val	Phe	Trp	Gly	
		180						185					190			
Val	Val	Lys	Gln	Ile	Gly	Gly	Leu	Val	Asp	Ala	Ile	Arg	Gly	Asp	Leu	
	195						200					205				
Val	Arg	Asp	Phe	Gly	Glu	Ser	Thr	Val	Glu	Val	Ile	Val	Thr	Gly	Gly	
	210					215					220					
Asn	Ser	Arg	Ile	Ile	Val	Pro	Glu	Ile	Gly	Pro	Val	Ser	Val	Ile	Asp	
225					230					235					240	
Glu	Leu	Ala	Val	Leu	Arg	Gly	Ser	Asp	Leu	Leu	Leu	Arg	Met	Asn	Met	
			245						250					255		

Pro

<210> 54
 <211> 774
 <212> DNA
 <213> Chlorobium tepidum

<400> 54

gtg	cgg	ctg	g	tcgtt	gac	at	cgg	caat	acc	agc	acg	acgt	tgg	cga	tttt	cacc	ggt	gat	60
gaag	agc	cgt	c	cggtc	gag	tc	ggt	acc	gag	t	gcgtt	gttt	ccg	att	ccag	caca	atg	cgc	120
gaag	tgt	ttt	g	gcaac	atg	gc	ccg	gaag	cac	ggc	gag	ccac	agg	ccat	cgc	catt	tg	cag	180
gtgg	tg	cct	t	ccg	tacc	gc	cg	tcg	gtt	cg	gcg	ttt	cgc	aat	cact	ttt	ctcc	gt	240
gtg	ctg	acca	t	ctg	ctg	taa	g	ctcc	gttt	t	c	tttt	ctg	t	cgact	acg	a	cccc	300
ac	ttc	ggc	g	cgg	atc	gc	ct	g	tg	cc	ctg	tg	gc	g	cat	ggag	cc	gac	360
ccg	gtt	atc	g	ccgtc	gatat	c	ggc	acg	gcc	at	cac	ctt	cg	ac	gtg	ctc	ga	cac	420
aatt	atc	gcg	g	gtgg	tct	cat	cat	gcc	gggt	at	cga	cat	ga	tgg	ccg	gag	c	gtt	480
aga	acc	gccc	g	agctt	cccc	a	ggt	gcg	cat	c	gac	agg	ccg	ag	agc	ctt	ct	cgg	540
acg	acc	gaat	g	cat	caaa	ag	cgg	agt	tttt	c	tggg	gag	tg	tcaa	acag	at	cgg	cgc	600
gtg	gac	gcc	a	ttc	gcg	gcg	a	ctt	gtac	gc	gact	ttg	gcg	agt	caac	ggt	cga	agt	660
gtc	acc	ggc	g	gcaat	agc	ag	gatt	atc	gtt	c	ccg	gag	atc	g	ccct	gtc	ag	tg	720
gaac	tcg	ctg	t	tcct	gcg	cg	cag	cga	tctt	t	ttg	ctg	cgg	a	tga	atg	gcc	gtga	774

<210> 55
 <211> 256
 <212> PRT
 <213> Clostridium difficile

<400> 55
 Met Leu Leu Val Phe Asp Val Gly Asn Thr Asn Met Val Leu Gly Ile
 1 5 10 15
 Tyr Lys Gly Asp Lys Leu Val Asn Tyr Trp Arg Ile Lys Thr Asp Arg
 20 25 30
 Glu Lys Thr Ser Asp Glu Tyr Gly Ile Leu Ile Ser Asn Leu Phe Asp
 35 40 45
 Tyr Asp Asn Val Asn Ile Ser Asp Ile Asp Asp Val Ile Ile Ser Ser
 50 55 60
 Val Val Pro Asn Val Met His Ser Leu Glu Asn Phe Cys Ile Lys Tyr
 65 70 75 80
 Cys Lys Lys Gln Pro Leu Ile Val Gly Pro Gly Ile Lys Thr Gly Leu
 85 90 95
 Asn Ile Lys Tyr Asp Asn Pro Lys Gln Val Gly Ala Asp Arg Ile Val
 100 105 110
 Asn Ala Val Ala Gly Ile Glu Lys Tyr Gly Ala Pro Ser Ile Leu Val
 115 120 125
 Asp Phe Gly Thr Ala Thr Thr Phe Cys Ala Ile Ser Glu Lys Gly Glu
 130 135 140
 Tyr Leu Gly Gly Thr Ile Ala Pro Gly Ile Lys Ile Ser Ser Glu Ala
 145 150 155 160
 Leu Phe Gln Ser Ala Ser Lys Leu Pro Arg Val Glu Leu Ala Lys Pro
 165 170 175
 Gly Met Thr Ile Cys Lys Ser Thr Val Ser Ala Met Gln Ser Gly Ile
 180 185 190
 Ile Tyr Gly Tyr Val Gly Leu Val Asp Lys Ile Ile Ser Ile Met Lys
 195 200 205
 Lys Glu Leu Asn Cys Asp Asp Val Lys Val Ile Ala Thr Gly Gly Leu
 210 215 220
 Ala Lys Leu Ile Ala Ser Glu Thr Lys Ser Ile Asp Tyr Val Asp Gly
 225 230 235 240
 Phe Leu Thr Leu Glu Gly Leu Arg Ile Ile Tyr Glu Lys Asn Gln Glu
 245 250 255

<210> 56
 <211> 771

<212> DNA

<213> *Clostridium difficile*

<400> 56

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atgcttctag tatttgatgt tggaaatact aatatggttt taggtatata taaaggtgac 60
aaattagtta attactggag aattaaaca gatagggaaa aaacgtctga tgaatatgga 120
atcctgataa gtaacctatt tgattatgat aatgtgaata taagtgatat tgatgatgtt 180
ataatatcat ctgtagttcc gaatgttatg cattctcttg aaaacttttg tataaagtac 240
tgtaaaaaac agccattaat agtaggtcca ggcataaaaa caggtctaaa tataaaatat 300
gataatccaa aacaagttgg ggcagataga atagttaatg ctgtagcagg gatagaaaag 360
tatggagcac caagtatact tgttgatttt ggaacagcaa ctacattttg tgctatctct 420
gaaaaagggtg aatatttggg tggacaata gcaccaggaa taaaaatc tagtgaggcg 480
ttatttcaaa gtgcgtctaa attacctaga gtagaattag ctaagccagg tatgactatt 540
tgtaagagta ctgtatcagc catgcaatct ggaataattt atggatatgt tggtttagtt 600
gacaaaataa taagtattat gaagaaagaa ttgaattgtg atgatgttaa ggttatagct 660
acagggtgat tagctaaact gattgcttca gagacgaaaa gtatagatta tgtagatggt 720
tttttaacac tagaaggatt gagaataata tatgaaaaaa accaagaata a 771
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<210> 57

<211> 219

<212> PRT

<213> *Dehalococcoides ethenogenes*

<400> 57

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Met Ser Glu Lys Leu Val Ala Val Asp Ile Gly Asn Thr Ser Val Asn
 1             5             10             15

Ile Gly Ile Phe Glu Gly Glu Lys Leu Leu Ala Asn Trp His Leu Gly
 20             25             30

Ser Val Ala Gln Arg Met Ala Asp Glu Tyr Ala Ser Leu Leu Leu Gly
 35             40             45

Leu Leu Gln His Ala Gly Ile His Pro Glu Glu Leu Asn Arg Val Ile
 50             55             60

Met Cys Ser Val Val Pro Pro Leu Thr Thr Thr Phe Glu Glu Val Phe
 65             70             75             80

Lys Ser Tyr Phe Lys Ala Ala Pro Leu Val Val Gly Ala Gly Ile Lys
 85             90             95

Ser Gly Val Lys Val Arg Met Asp Asn Pro Arg Glu Val Gly Ala Asp
100             105             110

Arg Ile Val Asn Ala Ala Ala Ala Arg Val Leu Tyr Pro Gly Ala Cys
115             120             125

Ile Ile Val Asp Met Gly Thr Ala Thr Thr Phe Asp Thr Leu Ser Glu
130             135             140

Gly Gly Ala Tyr Ile Gly Gly Ala Ile Ala Pro Gly Ile Ala Thr Ser
145             150             155             160

Ala Gln Ala Ile Ala Glu Lys Thr Ser Lys Leu Pro Lys Ile Glu Ile
165             170             175
```

Ile Arg Pro Ala Lys Val Ile Gly Ser Asn Thr Val Ser Ala Met Gln
180 185 190

Ser Gly Ile Tyr Phe Gly Tyr Ile Gly Leu Val Glu Glu Leu Val Arg
195 200 205

Arg Ile Gln Thr Glu Leu Gly Gln Lys Thr Arg
210 215

<210> 58

<211> 659

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 58

atgtctgaaa aactggtggc ggtagatatc ggcaatacca gcgtaaatat aggtatatatt 60
gagggcgaaa aactgctggc aaactggcat ctgggttcgg ttgccagcg tatggctgat 120
gaatatgcca gtctgtcttt aggcctgttg cagcacgccg gtatacaccc ggaagagcta 180
aacagggtaa tcatgtgcag tgttggtgcg cccctgacca ctacttttga agaggtattt 240
aaaagctatt tcaaggctgc tcctctggta gtgggtgcag gtataaagag cggggttaag 300
gtgcgcatgg ataacccccg tgaggttggg gctgaccgca tagtaaatgc cgctgccgcc 360
agggtgcttt atccgggggc gtgcataata gtggacatgg gtacggccac tacctttgat 420
accctttccg aggggtggggc atatataggc ggggcgattg caccgggtat tgccacctca 480
gccagggcta ttgcggaaaa gacttcaaaa ctgcccaaga ttgagataat ccgtcctgcc 540
aaagttatcg gctctaatac tgtgtcgggt atgcagtcag gtatatactt cggttatatc 600
gggctggtgg aagagctggt caggcggatt caaactgaat tggggcagaa aaccagagt 659

<210> 59

<211> 212

<212> PRT

<213> Desulfovibrio vulgaris

<400> 59

Met Thr Gln His Phe Leu Leu Phe Asp Ile Gly Asn Thr Asn Val Lys
1 5 10 15

Ile Gly Ile Ala Val Glu Thr Ala Val Leu Thr Ser Tyr Val Leu Pro
20 25 30

Thr Asp Pro Gly Gln Thr Thr Asp Ser Ile Gly Leu Arg Leu Leu Glu
35 40 45

Val Leu Arg His Ala Gly Leu Gly Pro Ala Asp Val Gly Ala Cys Val
50 55 60

Ala Ser Ser Val Val Pro Gly Val Asn Pro Leu Ile Arg Arg Ala Cys
65 70 75 80

Glu Arg Tyr Leu Tyr Arg Lys Leu Leu Phe Ala Pro Gly Asp Ile Ala
85 90 95

Ile Pro Leu Asp Asn Arg Tyr Glu Arg Pro Ala Glu Val Gly Ala Asp
100 105 110

Arg Leu Val Ala Ala Tyr Ala Ala Arg Arg Leu Tyr Pro Gly Pro Arg
 115 120 125
 Ser Leu Val Ser Val Asp Phe Gly Thr Ala Thr Thr Phe Asp Cys Val
 130 135 140
 Glu Gly Gly Ala Tyr Leu Gly Gly Leu Ile Cys Pro Gly Val Leu Ser
 145 150 155 160
 Ser Ala Gly Ala Leu Ser Ser Arg Thr Ala Lys Leu Pro Arg Ile Ser
 165 170 175
 Leu Glu Val Glu Glu Asp Ser Pro Val Ile Gly Arg Ser Thr Thr Thr
 180 185 190
 Ser Leu Asn His Gly Phe Ile Phe Gly Phe Ala Ala Met Thr Glu Gly
 195 200 205
 Val Leu Ala Ala
 210

<210> 60
 <211> 639
 <212> DNA
 <213> *Desulfovibrio vulgaris*

<400> 60
 atgaccagc atttcctgct gttcgacatc ggcaacacca acgtcaagat cggcatcgcg 60
 gtggaaccg ccgtgctgac ttcgtacgtg ctgcccacag accccggcca gacgaccgac 120
 tccatcgggc tgcgcctgct ggaggtgctg cgccatgccg ggctgggacc ggcggacgtg 180
 ggggcctgcg tggccagttc ggtggtgccc ggcgtaacc cgctgatccg ccgcgcctgc 240
 gaacgttacc tgtatcgcaa gctgctgttc gccccggcg acatcgccat tccgctggac 300
 aaccgctacg aacggcccgc cgaagtgggc gcggaccggc tgggtggcgc ctatgccgcc 360
 cggcggtgt accccggccc ccggtcgctg gtatccgtgg atttcggcac cgccaccacg 420
 tttgactgcg tggaagggg tgcgtatctt ggtggtttga tctgtcccgg cgtgctgtcg 480
 tccgcgggg cgttgtcgtc gcgcacggcc aagctgccgc gcatcagtct ggaagtggaa 540
 gaggattcgc cggtcacatcg gcggtccacc accaccagcc tgaaccacgg cttcattttc 600
 ggctttgccg ccatgaccga aggggtgctg gccgcctga 639

<210> 61
 <211> 249
 <212> PRT
 <213> *Pseudomonas putida*

<400> 61
 Met Ile Leu Glu Leu Asp Cys Gly Asn Ser Phe Ile Lys Trp Arg Val
 1 5 10 15
 Ile His Val Ala Asp Ala Val Ile Glu Gly Gly Gly Ile Val Asp Ser
 20 25 30
 Asp Gln Ala Leu Val Ala Glu Val Ala Ala Leu Ala Ser Val Arg Leu
 35 40 45
 Thr Gly Cys Arg Ile Val Ser Val Arg Ser Glu Glu Glu Thr Asp Ala

50	55	60
Leu Cys Ala Leu Ile Ala Gln Ala Phe Ala Val Gln Ala Lys Val Ala		
65	70	75 80
His Pro Val Arg Glu Met Ala Gly Val Arg Asn Gly Tyr Asp Asp Tyr		
	85	90 95
Gln Arg Leu Gly Met Asp Arg Trp Leu Ala Ala Leu Gly Ala Phe His		
	100	105 110
Leu Ala Lys Gly Ala Cys Leu Val Ile Asp Leu Gly Thr Ala Ala Lys		
	115	120 125
Ala Asp Phe Val Ser Ala Asp Gly Glu His Leu Gly Gly Tyr Ile Cys		
	130	135 140
Pro Gly Met Pro Leu Met Arg Ser Gln Leu Arg Thr His Thr Arg Arg		
	145	150 155 160
Ile Arg Tyr Asp Asp Ala Ser Ala Glu Arg Ala Leu Ser Ser Leu Ser		
	165	170 175
Pro Gly Arg Ser Thr Val Glu Ala Val Glu Arg Gly Cys Val Leu Met		
	180	185 190
Leu Gln Gly Phe Ala Tyr Thr Gln Leu Glu Gln Ala Arg Val Leu Trp		
	195	200 205
Gly Glu Glu Phe Thr Val Phe Leu Thr Gly Gly Asp Ala Pro Leu Val		
	210	215 220
Arg Ala Ala Leu Pro Gln Ala Arg Val Val Pro Asp Leu Val Phe Val		
	225	230 235 240
Gly Leu Ala Met Ala Cys Pro Leu Asp		
	245	

<210> 62
 <211> 750
 <212> DNA
 <213> Pseudomonas putida

<400> 62
 atgattcttg agctcgattg cggtaacagc ttcatacaagt ggcgggtgat ccatgttgcc 60
 gatgctgtga ttgaagggtg tgggatcgtc gattccgata aggcgctggt ggcggaagtg 120
 gctgcgctcg cttcagtgcg tctcacgggt tgccgtattg tcagtgtgcg cagcgaagaa 180
 gagaccgatg cgctttgcgc gttgattgct caggcatttg ccgtgcaggc gaaggttgcc 240
 caccctgtcc gtgaaatggc aggtgtgcgc aatggctatg acgactatca gcgcctgggt 300
 atggatcggt ggctggcggc gttgggggca tttcacctgg ccaagggcgc gtgcctggtg 360
 attgacctgg gtaccgcggc aaaagcggac ttcgtttctg cagatggcga gcatcttggg 420
 ggctacatct gccaggtat gccattgatg cgtagccagc tgcgcactca caccgcgcg 480
 atccgctatg acgatgcctc cgcgagcgc gcattgagca gcttgtcacc aggtcgctcg 540
 actgtcgaag cggtagagcg cggttgcgta ttgatgctcc agggctttgc ctacacccag 600
 cttgagcagg ctcgtgtgct atggggtgag gagttcaccg tggtcctcac tggcggtgat 660

gcgccactgg tgagggcggc cctgccacag gcgcgggtcg tgcctgacct ggttttcggt 720
 ggccctggcaa tggtttgtcc attggattga 750

<210> 63
 <211> 241
 <212> PRT
 <213> Thiobacillus ferrooxidans

<400> 63
 Met Ile Phe Ile Ala Val Gly Asn Thr Arg Thr Leu Leu Ala His Thr
 1 5 10 15
 His Asp Gly Val His Phe Asp Ser Val Ser Val Ala Thr Ser Leu Pro
 20 25 30
 Pro Thr Glu Ile Leu Gln Gln Pro Gly Leu Thr Trp Leu Ser Ala Pro
 35 40 45
 Asn Arg Glu Pro Val Ala Leu Gly Gly Val Val Pro Ala Ala Leu Ala
 50 55 60
 Ala Trp Arg Glu Ala Leu Ala Thr Ala Glu Val Arg Glu Pro Asp Pro
 65 70 75 80
 Gly Phe Phe Arg Arg Ala Val Pro His Asp Tyr His Pro Pro Glu Ser
 85 90 95
 Leu Gly Phe Asp Arg Arg Cys Cys Leu Leu Ala Ala Ala Met Asp Tyr
 100 105 110
 Pro Gly Gln Asp Ser Ile Val Ile Asp Met Gly Thr Ala Ile Thr Ile
 115 120 125
 Asp Leu Leu Ala Gly Gly His Phe Arg Gly Gly Arg Ile Leu Pro Gly
 130 135 140
 Ile Ala Met Ser Leu Arg Gly Leu His Glu Gly Thr Ala Leu Leu Pro
 145 150 155 160
 Glu Val Val Leu Asn Ala Pro Ala Glu Met Leu Gly Asn Asp Thr Ser
 165 170 175
 Asn Ala Ile Gln Ala Gly Val Ile His Leu Phe Ala Asp Ala Leu Arg
 180 185 190
 Gly Ala Ile Thr Asp Phe Arg Gln Tyr Ser Pro Gln Ala Arg Ile Leu
 195 200 205
 Ile Thr Gly Gly Asp Ala Glu Arg Trp Gln Pro Gly Ile Ala Gly Ser
 210 215 220
 Leu Tyr Gln Pro His Leu Leu Leu Arg Gly Phe Tyr Leu Trp Ile Arg
 225 230 235 240
 Gly

<210> 64
 <211> 726
 <212> DNA
 <213> *Thiobacillus ferrooxidans*

<400> 64
 atgatcttca tcgccgtcgg caataccgcg accctgctgg cacacacca cgatggcgtg 60
 catttcgaca gcgtcagcgt ggccacttcg ctgccacca cggaaatcct gcagcagccc 120
 ggcttgacat ggctcagcgc gccgaaccgg gaaccgcgtg cgctgggagg cgtcgtacct 180
 gcggcgcttg ccgcctggcg ggaagccttg gccacggcag aggtccgcga acccgacccc 240
 ggcttttttc gccgcgccgt gccgcacgac tatcatccgc cggaaagcct cggctttgac 300
 cgccgttgct gcctgctcgc cgccgccatg gactacccc gccaggacag catcgtcatc 360
 gacatgggca ccgccatcac catcgacctg ctggctggcg gacatttcg gggcggacgc 420
 attctgccgg gtatcgccat gagcctgcgc ggtctgcatg aaggcacggc actccttcct 480
 gaagtgcgtc tgaacgcccc agcggaaatg ctgggcaatg acaccagcaa cgccattcag 540
 gccggggtca tccacctctt tgccgatgcc ctgcgcggcg ccattaccga ctttcgccag 600
 tacagcccc aggcacggat actgatcacc ggtggcgatg ccgaacgttg gcaaccggcg 660
 atcgttggtg gcctgtacca gcccacatctg cttctgcgcg gcttttatct gtggatacgg 720
 ggatga 726

<210> 65
 <211> 242
 <212> PRT
 <213> *Xylessa fastidiosa*

<400> 65
 Met Asn Asp Trp Leu Phe Asp Leu Gly Asn Ser Arg Phe Lys Cys Ala
 1 5 10 15
 Ser Leu Arg Glu Gly Val Ile Gly Pro Val Thr Val Leu Pro Tyr Leu
 20 25 30
 Thr Glu Thr Met Asp Ala Phe Ala Leu Gln Glu Leu Pro Arg Gly Arg
 35 40 45
 Val Ala Tyr Leu Ala Ser Val Ala Ala Pro Ala Ile Thr Thr His Val
 50 55 60
 Leu Glu Val Leu Lys Ile His Phe Glu Gln Val Gln Val Ala Ala Thr
 65 70 75 80
 Val Ala Ala Cys Ala Gly Val Arg Ile Ala Tyr Ala His Pro Glu Arg
 85 90 95
 Phe Gly Val Asp Arg Phe Leu Ala Leu Leu Gly Ser Tyr Gly Glu Gly
 100 105 110
 Asn Val Leu Val Val Gly Val Gly Thr Ala Leu Thr Ile Asp Leu Leu
 115 120 125
 Ala Ala Asn Gly Cys His Leu Gly Gly Arg Ile Ser Ala Ser Pro Thr
 130 135 140
 Leu Met Arg Gln Ala Leu His Ala Arg Ala Glu Gln Leu Pro Leu Ser
 145 150 155 160

Gly Gly Asn Tyr Leu Glu Phe Ala Glu Asp Thr Glu Asp Ala Leu Val
 165 170 175
 Ser Gly Cys Asn Gly Ala Ala Val Ala Leu Ile Glu Arg Ser Leu Tyr
 180 185 190
 Glu Ala His Gln Arg Leu Asp Gln Ser Val Arg Leu Leu Leu His Gly
 195 200 205
 Gly Gly Val Ala Ser Leu Leu Pro Trp Leu Gly Asp Val Val His Arg
 210 215 220
 Pro Thr Leu Val Leu Asp Gly Leu Ala Ile Trp Ala Ala Val Ala Ala
 225 230 235 240
 Asn Val

<210> 66
 <211> 729
 <212> DNA
 <213> Xylella fastidiosa

<400> 66
 atgaatgatt gggtattcga tctaggtaat tcgcgtttta aatgtgcatc gctcagggaa 60
 ggtgtgattg gtccgtgaac gggtttgccg tacttaacag agaccatgga cgcgtttgcg 120
 ttacaggagc taccacgtgg tcgtgtggct tacttggcga gtgtcgctgc tccggctatt 180
 actacacatg tgctcgaagt attaaaaatc cacttcgagc aagtcaggt ggctgcaacc 240
 gtcgctgcat gtgccggagt acgaattgcc tatgtcacc cggaacgttt tggagtggat 300
 aggttcttag cgttgcttgg ttcgtatggt gagggcaatg tcctggtagt ggggtgctggg 360
 acagcattga ctattgattt gttggctgcc aatggttgtc atctcgagg gcgtatcagt 420
 gcttcaccga cattgatgcg ccaagcggtg catgcacgcg cgagcaact cccctcagt 480
 ggtgggaact acttgaggtt tgccgaagat acagaggatg cgttggtgtc agggtgcaat 540
 ggtgcagcgg tggcattgat cgaacgtagc ctgtatgagg cacatcaacg tttggaccag 600
 tcggttcgat tattgttgca tgggtggagg gtagcatctt tattgccttg gttgggcgac 660
 gtggtacatc gtcctacatt agtattggat ggctggcga tctgggctgc cgttgcagct 720
 aacgttttag 729

<210> 67
 <211> 223
 <212> PRT
 <213> Helicobacter pylori

<400> 67
 Met Pro Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys
 1 5 10 15
 Asp Ile Gly Asn Thr Arg Ile His Phe Ala Gln Asn Tyr Gln Leu Phe
 20 25 30
 Ser Ser Ala Lys Glu Asp Leu Lys Arg Leu Gly Ile Gln Lys Glu Ile
 35 40 45
 Phe Tyr Ile Ser Val Asn Glu Glu Asn Glu Lys Ala Leu Leu Asn Cys
 50 55 60

Tyr Pro Asn Ala Lys Asn Ile Ala Gly Phe Phe His Leu Glu Thr Asp
 65 70 75 80
 Tyr Val Gly Leu Gly Ile Asp Arg Gln Met Ala Cys Leu Ala Val Asn
 85 90 95
 Asn Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile Asp Leu Ile
 100 105 110
 Lys Glu Gly Lys His Leu Gly Gly Cys Ile Leu Pro Gly Leu Ala Gln
 115 120 125
 Tyr Ile His Ala Tyr Lys Lys Ser Ala Lys Ile Leu Glu Gln Pro Phe
 130 135 140
 Lys Ala Leu Asp Ser Leu Glu Val Leu Pro Lys Ser Thr Arg Asp Ala
 145 150 155 160
 Val Asn Tyr Gly Met Val Leu Ser Val Ile Ala Cys Ile Gln His Leu
 165 170 175
 Ala Lys Asn Gln Lys Ile Tyr Leu Cys Gly Gly Asp Ala Lys Tyr Leu
 180 185 190
 Ser Ala Phe Leu Pro His Ser Val Cys Lys Glu Arg Leu Val Phe Asp
 195 200 205
 Gly Met Glu Ile Ala Leu Lys Lys Ala Gly Ile Leu Glu Cys Lys
 210 215 220

<210> 68
 <211> 672
 <212> DNA
 <213> *Helicobacter pylori*

<400> 68
 atgccagcta ggcaatcttt tacagatttg aaaaacctgg ttttgtgcga tataggcaac 60
 acgcgtatcc attttgcaca aaactatcag ctcttttcaa gcgctaaaga agattttaaag 120
 cgtttggtta ttcaaaagga aattttttac attagcgtga atgaagaaaa tgaaaaagcc 180
 cttttgaatt gttaccctaa cgctaaaaat attgcagggt tttttcattt agaaaccgac 240
 tatgtagggc ttgggataga ccggcaaagt gcgtgtcttg cggtaaataa tggcgtggtg 300
 gtggatgccg ggagtgcgat tacgatagat ttaatcaaag agggcaagca tttaggaggg 360
 tgtattttac ccggttttagc ccaatatatt catgcgtata aaaaaagcgc taaaatttta 420
 gagcaacctt tcaaggcctt agattcttta gaagttttac ctaaaagcac tagagacgct 480
 gtgaattacg gcatggtttt gagcgtcatt gcttgatcc agcatttagc caaaaatcaa 540
 aaaatctatc tttgtggggg cgatgcgaag tatttgagcg cgtttttacc ccattctgtt 600
 tgcaaggagc gtttggtttt tgacgggatg gaaatcgctc ttaaaaaagc aggatacta 660
 gaatgcaaat ga 672

<210> 69
 <211> 750
 <212> DNA
 <213> *Pseudomonas syringae*

<400> 69

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atgattcttg agctcgattg cggcaacagc tttatcaagt ggcggataat cacaaagagt 60
tgctcaacgt tggtcagcgg cggagtagtg gactcggaca cagccttgct agagtgcctg 120
ggcaatctgt caggcgagc attcagcgat tgccgtctgg taagcggtcg tagcgcgga 180
gaaacggcga agctggtttg cgcgctggca gatacctttt ccattagccc tgtctgtgca 240
gcgccggcgc cagagcttgc cggggtaatc aatggatacg acgattttgc acgcttgggg 300
ctggatcgct ggttggcatt tgtaggggct taccaccttg ttaaggggtgc ctgcctgggt 360
atcgatctgg gcaccgccat tacgtctgac tttgttgaag cgtcaggaaa gcatctgggt 420
ggtttcatct gtcctggcat gccactgatg cgcaatcagc tgcgtacca caccgcgcgc 480
attcgatatg acgatgcaga ggctgaaaaa gccctggtac gactcgtgcc tggccgtgcg 540
acggccgagg ctgtggagcg aggttgttct ctcatgcttc gcggattcgc aatgactcag 600
atcgagatag ctcgcgaata ctggggggac gactttgcta ttttcgtgac aggagggcag 660
gctgtcttgg ttgctgatgt gttaccgggc gctcgcattg tccctgattt ggtattcgtt 720
ggcctggctc tcgcttgccc ttacgttga 750

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<210> 70

<211> 249

<212> PRT

<213> *Pseudomonas syringae*

<400> 70

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Met Ile Leu Glu Leu Asp Cys Gly Asn Ser Phe Ile Lys Trp Arg Ile
 1             5             10             15

Ile Thr Lys Ser Cys Ser Thr Leu Val Ser Gly Gly Val Val Asp Ser
      20             25             30

Asp Thr Ala Leu Leu Glu Cys Leu Gly Asn Leu Ser Gly Ala Ala Phe
      35             40             45

Ser Asp Cys Arg Leu Val Ser Val Arg Ser Ala Glu Glu Thr Ala Lys
      50             55             60

Leu Val Cys Ala Leu Ala Asp Thr Phe Ser Ile Ser Pro Val Cys Ala
      65             70             75             80

Ala Pro Ala Pro Glu Leu Ala Gly Val Ile Asn Gly Tyr Asp Asp Phe
      85             90             95

Ala Arg Leu Gly Leu Asp Arg Trp Leu Ala Phe Val Gly Ala Tyr His
      100            105            110

Leu Val Lys Gly Ala Cys Leu Val Ile Asp Leu Gly Thr Ala Ile Thr
      115            120            125

Ser Asp Phe Val Glu Ala Ser Gly Lys His Leu Gly Gly Phe Ile Cys
      130            135            140

Pro Gly Met Pro Leu Met Arg Asn Gln Leu Arg Thr His Thr Arg Arg
      145            150            155            160

Ile Arg Tyr Asp Asp Ala Glu Ala Glu Lys Ala Leu Val Arg Leu Val
      165            170            175

Pro Gly Arg Ala Thr Ala Glu Ala Val Glu Arg Gly Cys Ser Leu Met
      180            185            190

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Leu Arg Gly Phe Ala Met Thr Gln Ile Glu Ile Ala Arg Glu Tyr Trp
 195 200 205
 Gly Asp Asp Phe Ala Ile Phe Val Thr Gly Gly Asp Ala Val Leu Val
 210 215 220
 Ala Asp Val Leu Pro Gly Ala Arg Ile Val Pro Asp Leu Val Phe Val
 225 230 235 240
 Gly Leu Ala Leu Ala Cys Pro Leu Arg
 245

<210> 71
 <211> 8320
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: plasmid, pAN296

<400> 71
 tgcgccgcta cagggcgcggt ccattcgcca ttcaggctgc gcaactgttg ggaagggcga 60
 tcggtgcggg cctcttcgct attacgccag ctggcgaaag ggggatgtgc tgcaaggcga 120
 ttaagttggg taacgccagg gttttccag tcacgacgtt gtaaaacgac ggccagtgaa 180
 ttgtaatacg actcactata gggcgaattg ggcccgacgt cgcattgctg atgaaaagcc 240
 gatgaccgct tttcaggctc gtcagcagct ttttcctgct gtatatgaaa aggaattgtt 300
 tttaacgatg tcagaaaacgg caggtcacct tgatgtgttg gaggctgaag aagccatcac 360
 gtcataattg gaaggaaata ccgtataact taaaacaatg aagaggtgaa atgggtgaaa 420
 catatagcgg gaaaaaggat ttggataacc ggcgcttcag gagggttgag agaaagaatc 480
 gcatacttat gcgcggctga aggagcccat gtcctgctgt cggctagacg cgaggatcgt 540
 ttgatagaaa tcaaaaggaa aataaccgag gaatggagcg gacagtgtga gatttttcct 600
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: plasmid, pAN341 and pAN342

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<223> Description of Artificial Sequence: plasmid, pAN329 and pAN330

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<210> 76

<211> 3859

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plasmid, pOTP72

<400> 76

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<210> 77

<211> 3934

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plasmid, pOTP73

<400> 77

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